

Kemmerer, Elizabeth

From: Kemmerer, Elizabeth
Sent: Thursday, June 19, 2003 2:29 PM
To: Kunz, Gary
Subject: SPDI favor

Importance: High

Hi Gary-

I am currently working on 09/941992, a SPDI case which is a date case. The 2 companion cases are not yet docketed: 09/990711 and 09/991150. They're both in central files on the 12th floor. Can these be docketed to me as well, since it would be easy to write up the 3 cases together, and they're all date cases?

Thanks a bunch,

Elizabeth (Betsy) Kemmerer
Art Unit 1646
308-2673
CM1-10B17
Mailbox: 10D19

STIC-Biotech/ChemLib

97031

From: Kemmerer, Elizabeth
Sent: Thursday, June 19, 2003 2:30 PM
To: STIC-Biotech/ChemLib
Subject: sequence search request

Please search SEQ ID NO: 20 for 09/941992; regular and interference, please.

Thanks,

Elizabeth (Betsy) Kemmerer
Art Unit 1646
308-2673
CM1-10B17
Mailbox: 10D19

CRBS

Mary Jane Kuhl
Tech. Info. Specialist, STIC
TC-1600
CM-1, Room 6A-06
Phone: 605-1155

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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:44:16 ; Search time 38 Seconds
(without alignments)
1606.021 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MWLRWALSPSSCLWAEPG.....DEASSGGSGTSDTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_101002.*

1: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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14: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2384	100.0	458	21	Human PRO341 prote
2	2384	100.0	458	22	Human PRO341 (UNQ3
3	2375	99.6	458	21	Membrane-bound pro
4	1816	76.2	374	19	Human secreted pro
5	1816	76.2	530	21	HTM clone 156986
6	1816	76.2	530	22	Human polypeptide,
7	1816	76.2	530	23	Human polypeptide
8	990	41.5	365	22	Human protein sequ
9	545.5	22.9	760	23	Human transporter
10	284	11.9	60	22	Human secreted pro

11	195	8.2	173	22	AA664947	Human secreted pro
12	157	6.6	479	22	AAU39678	Propionibacterium
13	143.5	6.0	457	19	AAW42430	Escherichia coli g
14	132	5.5	443	21	AAW86230	Human secreted pro
15	131	5.5	433	22	AAE10448	Human transmembran
16	131	5.5	451	22	AAE10450	Human transmembran
17	131	5.5	480	22	AAE10445	Human transmembran
18	131	5.5	480	23	AAE22919	Human transporter
19	128.5	5.4	456	10	AAU91895	Protein sequence o
20	126.5	5.3	460	22	AAU98416	Escherichia coli p
21	123	5.2	1281	22	AAE00308	Dog P-glycoprotein
22	123	5.2	1281	22	AAE00309	Dog P-glycoprotein
23	123	5.2	1281	22	AAE00310	Dog P-glycoprotein
24	122	5.1	1281	22	AAE00303	Dog (PGP) P-glycop
25	121.5	5.1	496	23	AAU96093	RhCW unique short
26	121	5.1	1280	22	AAE1068	Dog P-glycoprotein
27	121	5.1	1280	22	AAE00304	Dog P-glycoprotein
28	119	5.0	490	23	ABE54849	Lactococcus lactis
29	118	4.9	872	23	ABG62165	Human prostate spe
30	112.5	4.7	95	22	AAU14913	Novel bone marrow
31	112.5	4.7	1280	22	AAU04347	Human multidrug re
32	112	4.7	260	22	AAE10449	Human transmembran
33	112	4.7	1005	22	ABG11447	Novel human diagno
34	111	4.7	457	21	AAU70516	Human BAG-4 protei
35	110.5	4.6	462	23	ABE55338	Lactococcus lactis
36	110.5	4.6	500	21	AAU71305	Human orphan G pro
37	110.5	4.6	500	21	AAU02839	Human G protein co
38	110	4.6	394	18	AAW20797	H. pylori transpor
39	110	4.6	1283	22	AAE1065	Cynomolgus monke
40	109	4.6	457	20	AAU30348	A suppressor of de
41	108.5	4.6	180	22	ABG12827	Novel human diagno
42	108.5	4.6	180	22	ABG14843	Novel human diagno
43	108.5	4.6	386	19	AAW98237	H. pylori GHPO 699
44	108.5	4.6	386	19	AAW71489	Helicobacter polyp
45	108	4.5	224	22	AAE10447	Human transmembran

ALIGNMENTS

RESULT 1

AAE24059

ID AAB24059 standard; Protein: 458 AA.

XX AAB24059;

XX 29-JAN-2001 (first entry)

XX Human PRO341 protein sequence SEQ ID NO:10.

XX Human: tumour; diagnosis: neoplastic disease; neoplastic cell growth;
KW proliferation; tumorigenesis; identification; cancer; cytostatic;
KW neurotropic; neuroprotective; antiinflammatory; immunosuppressive;
KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
KW neuronal disorder; gliad disorder; astrocytal disorder; angiogenic;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; stromal disorder; blastocoele disorder;
KW inflammatory disorder; immunologic disorder.

XX Homo sapiens.

XX WO200053755-A2.

XX 14-SEP-2000.

XX 06-JAN-2000; 2000WO-US00376.

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 30-NOV-1999; 99WO-US28313.

PR	02-JUN-1998	98US-0087609
PR	02-JUN-1998	98US-0087759
PR	03-JUN-1998	98US-0088287
PR	04-JUN-1998	98US-0088021
PR	04-JUN-1998	98US-0088025
PR	04-JUN-1998	98US-0088028
PR	04-JUN-1998	98US-0088029
PR	04-JUN-1998	98US-0088030
PR	04-JUN-1998	98US-0088033
PR	04-JUN-1998	98US-0088326
PR	05-JUN-1998	98US-0088167
PR	05-JUN-1998	98US-0088202
PR	05-JUN-1998	98US-0088212
PR	05-JUN-1998	98US-0088217
PR	09-JUN-1998	98US-0088655
PR	10-JUN-1998	98US-0088722
PR	10-JUN-1998	98US-0088730
PR	10-JUN-1998	98US-0088734
PR	10-JUN-1998	98US-0088738
PR	10-JUN-1998	98US-0088740
PR	10-JUN-1998	98US-0088741
PR	10-JUN-1998	98US-0088742
PR	10-JUN-1998	98US-0088810
PR	10-JUN-1998	98US-0088811
PR	10-JUN-1998	98US-0088824
PR	10-JUN-1998	98US-0088825
PR	10-JUN-1998	98US-0088826
PR	11-JUN-1998	98US-0088858
PR	11-JUN-1998	98US-0088863
PR	11-JUN-1998	98US-0088865
PR	11-JUN-1998	98US-0088876
PR	12-JUN-1998	98US-0089090
PR	12-JUN-1998	98US-0089105
PR	16-JUN-1998	98US-0089440
PR	16-JUN-1998	98US-0089512
PR	16-JUN-1998	98US-0089514
PR	17-JUN-1998	98US-0089532
PR	17-JUN-1998	98US-0089538
PR	17-JUN-1998	98US-0089598
PR	17-JUN-1998	98US-0089599
PR	17-JUN-1998	98US-0089600
PR	17-JUN-1998	98US-0089653
PR	18-JUN-1998	98US-0089801
PR	18-JUN-1998	98US-0089907
PR	18-JUN-1998	98US-0089908
PR	19-JUN-1998	98US-0089947
PR	19-JUN-1998	98US-0089948
PR	21-JUN-1998	98US-0089952
PR	22-JUN-1998	98US-0090246
PR	22-JUN-1998	98US-0090252
PR	22-JUN-1998	98US-0090254
PR	23-JUN-1998	98US-0090349
PR	23-JUN-1998	98US-0090355
PR	24-JUN-1998	98US-0090429
PR	24-JUN-1998	98US-0090431
PR	24-JUN-1998	98US-0090435
PR	24-JUN-1998	98US-0090444
PR	24-JUN-1998	98US-0090445
PR	24-JUN-1998	98US-0090461
PR	24-JUN-1998	98US-0090472
PR	24-JUN-1998	98US-0090535
PR	24-JUN-1998	98US-0090538
PR	24-JUN-1998	98US-0090540
PR	24-JUN-1998	98US-0090557
PR	25-JUN-1998	98US-0090676
PR	25-JUN-1998	98US-0090678
PR	25-JUN-1998	98US-0090688
PR	25-JUN-1998	98US-0090690
PR	25-JUN-1998	98US-0090691
PR	25-JUN-1998	98US-0090694
PR	25-JUN-1998	98US-0090695
PR	25-JUN-1998	98US-0090696
PR	26-JUN-1998	98US-0090862

XX Birse CE, Rosen CA;
 XX WPI: 2002-122018/16.
 DR N-PSDB; ABL90743.
 XX Novel 1405 isolated polypeptides, useful for diagnosis, treatment and
 PT prevention of neural, immune system, muscular, reproductive,
 PT gastrointestinal, pulmonary, cardiovascular, renal and proliferative
 PT disorders -
 XX Claim 11: SEQ ID NO 2710; 208lpp + Sequence Listing; English.
 XX The invention relates to novel genes (ABL9449-ABL90853) and proteins
 CC (ABB90440-ABB90444) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
 CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
 CC and ovarian cancer and other cancers of the adrenal gland, bone, bone
 CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital;
 CC (b) immune disorders e.g. Addison's disease, allergies, autoimmune
 CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
 CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
 CC colitis; (c) cardiovascular disorders such as myocardial ischaemias;
 CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and
 CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
 CC and parasitic infections.
 CC Note: The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 530 AA;
 * Query Match 76.2%; Score 1816; DB 23; Length 530;
 Best Local Similarity 94.3%; Pred. No. 3.8e-163;
 Matches 362; Conservative 5; Mismatches 5; Indels 12; Gaps 2;
 Qy 75 TCFSIASLKOWSRVSMFPTRLSPCSSATEQTERDSATAYRMVTEVLGTALGQIIVG 134
 Db 159 TCFHV----PYSALTME-----ISTEQTERDSATAYRMVTEVLGTALGQIIVG 206
 Qy 135 QADTPCFQDPSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 194
 Db 207 QADTPCFQDLSNSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 266
 Qy 195 QREPYEAQOSEPIAYFRGLRLVMSHGPIYKLIITGFLFTSLAFMLVGNFVLCFTYTLGFR 254
 Db 267 QREPYEAQOSEPIAYFRGLRLVMSHGPIYKLIITGFLFTSLAFMLVGNFVLCFTYTLGFR 326
 Qy 255 NEFQNLALLMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIIITYA 314
 Db 327 NEFQNLALLMLSATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVALMESNLIIITYA 386
 Qy 315 VAVAAGISVAFAFLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYFFFTKFSAGSVSLGIS 374
 Db 387 VAVAAGISVAFAFLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYFFFTKFSAGSVSLGIS 446
 Qy 375 TSLDFAGYQTRGCSQPERVKFTLNMLVTMAPVLVILGLLLFKMYPIDERRRQNKAL 434
 Db 447 TSLDFAGYQTRGCSQPERVKFTLNMLVTMAPVLVILGLLLFKMYPIDERRRQNKAL 506
 Qy 435 QALRDEASSSSGCSFDTSTELASIL 458
 Db 507 QALRDEASSSSGCSFDTSTELASIL 530
 RESULT 8
 AAB94114
 ID AAB94114 standard; Protein: 365 AA.
 XX
 AC AAB94114;
 XX

DT 26-JUN-2001 (first entry)
 XX Human protein sequence SEQ ID NO:14354.
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX Homo sapiens.
 XX EP1074617-A2.
 XX 07-FEB-2001.
 XX 28-JUL-2000; 2000EP-0116126.
 XX 29-JUL-1999; 99JP-0248036.
 XX 27-AUG-1999; 99JP-0300253.
 XX 11-JAN-2000; 2000JP-0118776.
 XX 02-MAY-2000; 2000JP-0183767.
 XX 09-JUN-2000; 2000JP-0241899.
 XX (HELI-) HELIX RES INST.
 XX Ota T, Isozaki T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX WPI: 2001-318749/34.
 XX Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX Claim 8; SEQ ID 14354; 2537pp + CD ROM; English.
 XX The present invention describes primer sets for synthesising 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX Sequence 365 AA;
 SQ
 Query Match 41.5%; Score 990; DB 22; Length 365;
 Best Local Similarity 90.0%; Pred. No. 3.8e-85;
 Matches 197; Conservative 5; Mismatches 5; Indels 12; Gaps 2;
 Qy 75 TCFSIASLKOWSRVSMFPTRLSPCSSATEQTERDSATAYRMVTEVLGTALGQIIVG 134
 Db 159 TCFHV----PYSALTME-----ISTEQTERDSATAYRMVTEVLGTALGQIIVG 206
 Qy 135 QADTPCFQDPSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 194
 Db 207 QADTPCFQDLSNSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIICAVILILGVRE 266
 Qy 195 QREPYEAQOSEPIAYFRGLRLVMSHGPIYKLIITGFLFTSLAFMLVGNFVLCFTYTLGFR 254
 XX

KW corneal graft neovascularisation; neurological disorder; regeneration;
 KW Huntington's chorea; Alzheimer's disease; Parkinson's disease;
 KW infectious disease; chemotaxis.
 OS Homo sapiens.
 XX WO200076530-A1.
 XX 21-DEC-2000.
 XX 01-JUN-2000; 2000WO-US14933.
 XX 11-JUN-1999; 99US-0138572.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.
 XX Rosen CA, Ruben SM, Komatsoulis GA;
 XX WPI; 2001-071147/08.
 DR N-PSDB; AAF33221.
 XX Nucleic acids encoding 49 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX Claim 11; Page 488; 554pp; English.
 XX The polynucleotide sequences given in AAF33213 to AAF33261 encode the
 CC human secreted proteins given in AAB64882 to AAB64930. AAB64931 to
 CC AAB64991 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC immunomodulatory; antisclerotic; dermatological; immunosuppressive;
 CC antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiac;
 CC vascular; antimicrobial; anti-angiogenic; ophthalmological;
 CC neuroprotectant; anticonvulsant; nootropic; antialzheimers;
 CC antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can
 CC be used in the prevention, diagnosis and treatment of diseases associated
 CC with inappropriate polypeptide expression. Disorders that may be
 CC prevented, diagnosed and/or treated by the above methods include immune
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
 CC human immuno-deficiency virus (HIV) infections), hyperproliferative
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
 CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft
 CC neovascularisation and diabetic retinopathy), neurological disorders
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
 CC infectious diseases and/or for promoting wound healing, regeneration and
 CC /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences
 CC used in the exemplification of the present invention.
 XX Sequence 60 AA;
 SQ Query Match 11.9%; Score 284; DB 22; Length 60;
 Best Local Similarity 100.0%; Pred. No. 2.5e-19;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 400 MLVTMAPIVLILGLLFLKMPIDERRRQNKALQALRDPASSGSGSETDSTELASIL 458
 Db 1 MLVTMAPIVLILGLLFLKMPIDERRRQNKALQALRDPASSGSGSETDSTELASIL 59

RESULT 11
 AAB64947
 ID AAB64947 standard; Protein; 173 AA.
 XX AAB64947;
 AC AAB64947;
 XX 23-MAR-2001 (first entry)
 DT Human secreted protein sequence encoded by gene 9 SEQ ID NO:125.
 XX

XX Human; secreted protein; diagnosis; immunomodulatory; antisclerotic;
 KW dermatological; immunosuppressive; antiinflammatory; anti-HIV;
 KW immunostimulant; cytostatic; cardiac; vascular; anti-angiogenic;
 KW ophthalmological; neuroprotectant; nootropic; anticonvulsant; vulnerary;
 KW antialzheimers; antiparkinsonian; antimicrobial; immune disorder;
 KW multiple sclerosis; systemic lupus erythematosus; HIV; infection;
 KW hyperproliferative disorder; cancer; Gaucher's disease; wound healing;
 KW cardiovascular disease; Scimitar syndrome; Chaga's cardiomyopathy;
 KW coronary arteriosclerosis; angiogenic disorder; diabetic retinopathy;
 KW corneal graft neovascularisation; neurological disorder; regeneration;
 KW Huntington's chorea; Alzheimer's disease; Parkinson's disease;
 KW infectious disease; chemotaxis.
 XX Homo sapiens.
 XX WO200076530-A1.
 XX 21-DEC-2000.
 XX 01-JUN-2000; 2000WO-US14933.
 XX 11-JUN-1999; 99US-0138572.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.
 XX Rosen CA, Ruben SM, Komatsoulis GA;
 XX WPI; 2001-071147/08.
 DR Nucleic acids encoding 49 human secreted polypeptides, useful for
 CC preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 CC disease and diabetic retinopathy -
 XX Disclosure; Page 525; 554pp; English.
 XX The polynucleotide sequences given in AAF33213 to AAF33261 encode the
 CC human secreted proteins given in AAB64882 to AAB64930. AAB64931 to
 CC AAB64991 represent human secreted polypeptide sequences and proteins
 CC homologous to them, which are given in the exemplification of the present
 CC invention. Human secreted proteins have activities based on the tissues
 CC and cells the genes are expressed in. Examples of activities include:
 CC immunomodulatory; antisclerotic; dermatological; immunosuppressive;
 CC antiinflammatory; anti-HIV; immunostimulant; cytostatic; cardiac;
 CC vascular; antimicrobial; anti-angiogenic; ophthalmological;
 CC neuroprotectant; anticonvulsant; nootropic; antialzheimers;
 CC antiparkinsonian; and vulnerary. The polynucleotides and polypeptides can
 CC be used in the prevention, diagnosis and treatment of diseases associated
 CC with inappropriate polypeptide expression. Disorders that may be
 CC prevented, diagnosed and/or treated by the above methods include immune
 CC disorders (e.g. multiple sclerosis, systemic lupus erythematosus and
 CC human immuno-deficiency virus (HIV) infections), hyperproliferative
 CC disorders (e.g. cancers and Gaucher's disease), cardiovascular diseases
 CC (e.g. Scimitar syndrome, Chaga's cardiomyopathy and coronary
 CC arteriosclerosis), angiogenic disorders (e.g. corneal graft
 CC neovascularisation and diabetic retinopathy), neurological disorders
 CC (e.g. Huntington's chorea, Alzheimer's disease and Parkinson's disease),
 CC infectious diseases and/or for promoting wound healing, regeneration and
 CC /or chemotaxis. AAF33204 to AAF33212 and AAB64881 represent sequences
 CC used in the exemplification of the present invention.
 XX Sequence 173 AA;
 SQ Query Match 8.2%; Score 195; DB 22; Length 173;
 Best Local Similarity 66.2%; Pred. No. 2.7e-10;
 Matches 43; Conservative 5; Mismatches 5; Indels 12; Gaps 2;
 QY 75 TCFESIASLKOWSRVSMPEPTRLSPCSSATEQTERDSATAYRMTVEVLGTVLCTAIOGQIVG 134
 Db 121 TCFHV----PYSALTMF-----ISTEQTERDSATAYRMTVEVLGTVLCTAIOGQIVG 168
 QY 135 QADTP 139

XX	Sequence	457 AA;	
Query Match	6.0%; Score 143.5; DB 19; Length 457;		
Best Local Similarity	19.8%; Pred. No. 7.5e-05;		
Matches	75; Conservative 62; Mismatches 178; Indels 63; Gaps 13		
QY	73 ICTCFSIASLQKQSRVSMFPRLSPCSSTAEOTEDRSATAYRMTVEVLGTGTAIQGOI	132	
Db	119 LGLCYSLNIPYGLSATAMTQQ--PQSRARLGAARGIAAS--LTFVCLAFLLGPSIK---	171	
QY	133 VQGAQTPCFQDFNSSTVASQSANHTGTTSHRETKQAYLLAAGVIVCIYIIICAVILLCV	192	
Db	172 -----NSSPEEMWVYH-----FWTIVLAIAGMV--LYPIC-----FKST	204	
QY	193 REQREPYEAQOSEPTAYRGLRLVMSHGPIKLTGFLFTSLAFMLVEGNFVLCTYTLG	252	
Db	205 RENVVRIVAQPSLNIS---LQTKRNRPLPMLCIGALCVLISTFAVSASSLFYVRYVLN	260	
QY	253 FNEFQNLALLAIMLSATL-TPIQWQFLTRFGKKTAYVVG-ISSAVPEFILILVALMESNLI	310	
Db	261 DTGLETFLVLQNLVGTVASAPLVPGMVARIGKKNFTLIGALLTGCYLLLFFWVSVMSLP	320	
QY	311 IITYAVAVAAGISVAFAFLLPMSMLPDVIDDFHLKQPHFG-----TEPIEFSEFVFT	363	
Db	321 VALVALATASIGQGVMTVMVALEADTVE-----YGEYLTGVRIEGLTYSLSFSEFR	371	
QY	364 KPAQSVSLGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPIVLILLGLLLEKWPID	423	
Db	372 KCGQAIGGSIAPFILLGLSGYIANQVQTPV-VIMGRTSIALVPCGFMLLAFVIINWFYPLT	430	
QY	424 EERRQ-----NKKALQ 435		
Db	431 DKKFKEIVVEIDNRKKVQ 448		
RESULT 14			
DAY86230			
DAY86230	standard; Protein; 443 AA.		
XX	AA86230;		
XX	19-APR-2000 (first entry)		
XX	Human secreted protein HKFBC53, SEQ ID NO:145.		
XX	Human; secreted protein; cancer; tumour; developmental abnormality;		
XX	fetal deficiency; blood disorder; immune system disorder; inflammation;		
XX	autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;		
XX	schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;		
XX	atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;		
XX	digestive disorder; endocrine disorder; infection; AIDS; leukaemia;		
XX	therapy.		
OS	Homo sapiens.		
XX	WO9966041-A1.		
XX	23-DEC-1999.		
XX	15-JUN-1999; 99WO-US13418.		
XX	16-JUN-1998; 98US-0089507.		
XX	16-JUN-1998; 98US-0089508.		
XX	16-JUN-1998; 98US-0089509.		
XX	16-JUN-1998; 98US-0089510.		
XX	22-JUN-1998; 98US-0090112.		
XX	22-JUN-1998; 98US-0090113.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
XX	Ruben SM, Ni J, Rosen CA, Wei Y, Young PE, Florence KA;		
PI	Soppet DR, Brewer LA, Endress GA, Carter KC, Mucenski M, Ebner R;		

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: June 19, 2003, 17:46:17 ; Search time 26 Seconds
(without alignments)
518.296 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MWLRWALSPLPSSCLWAEFG.....DEASSSGCSETDSTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCFUS.COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	143.5	6.0	457	2	US-08-882-704A-6
2	143.5	6.0	457	4	US-09-151-957-6
3	128.5	5.4	456	6	5432081-7
4	120.5	5.1	428	6	5432081-9
5	109	4.6	457	3	US-09-416-213-2
6	109	4.6	457	4	US-09-416-214-2
7	109	4.6	457	4	US-09-035-676-2
8	107.5	4.5	1280	2	US-08-752-447-2
9	107.5	4.5	1280	4	US-09-316-167-2
10	107	4.5	426	6	5268463-8
11	106.5	4.5	1280	2	US-08-583-276-19
12	106.5	4.5	1280	6	5206352-4
13	106	4.4	580	2	US-08-677-049-12
14	103	4.3	457	6	5268463-7
15	101	4.2	460	1	US-08-689-974-5
16	101	4.2	460	3	US-09-058-376-5
17	97.5	4.1	822	4	US-08-684-932A-38
18	96.5	4.0	364	5	PCT-US96-10618-2
19	96	4.0	1279	2	US-08-784-649A-2
20	95.5	4.0	445	4	US-09-134-001C-3507
21	95	4.0	435	6	5268463-9
22	95	4.0	436	6	5432081-10
23	94.5	4.0	290	4	US-09-134-001C-4893
24	93.5	3.9	369	4	US-09-172-353-6
25	93.5	3.9	384	4	US-09-200-673-15
26	93	3.9	808	4	US-09-134-001C-3105
27	92.5	3.9	383	3	US-09-045-186-2

28	92.5	3.9	384	1	US-08-232-144-4	Sequence 4, Appli
29	92.5	3.9	384	2	US-08-555-268A-15	Sequence 15, Appli
30	92.5	3.9	384	5	PCT-US93-05039-3	Sequence 3, Appli
31	92.5	3.9	765	2	US-08-846-762-5	Sequence 5, Appli
32	92	3.9	364	4	US-08-763-938-2	Sequence 2, Appli
33	91	3.8	640	4	US-09-627-376-16	Sequence 16, Appli
34	91	3.8	683	4	US-09-134-001C-5576	Sequence 5576, Ap
35	91	3.8	878	4	US-09-556-706B-2	Sequence 2, Appli
36	91	3.8	907	3	US-08-783-774-2	Sequence 1, Appli
37	91	3.8	907	4	US-09-328-599A-1	Sequence 1, Appli
38	91	3.8	907	5	PCT-US95-04611A-19	Sequence 19, Appli
39	89.5	3.8	404	1	US-08-696-770-2	Sequence 2, Appli
40	89.5	3.8	404	2	US-09-015-557-2	Sequence 2, Appli
41	89.5	3.8	540	4	US-09-513-057C-33	Sequence 33, Appli
42	88.5	3.7	462	2	US-08-898-976-2	Sequence 2, Appli
43	88.5	3.7	462	2	US-08-898-976-4	Sequence 4, Appli
44	88	3.7	382	1	US-08-415-818-7	Sequence 7, Appli
45	88	3.7	382	2	US-08-894-236-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-08-882-704A-6
; Sequence 6, Application US/08882704A
; Patent No. 5879906
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Wilson, Katherine J.
; APPLICANT: Leader, Michael
; TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,704A
; FILING DATE: 25-JUN-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5879906tenburg Ph.D., Carol
; REGISTRATION NUMBER: 39,317
; REFERENCE/DOCKET NUMBER: 190106.404
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-882-704A-6

Query Match 6.0%; Score 143.5; DB 2; Length 457;
Best Local Similarity 19.8%; Pred. No. 2.le-05;
Matches 75; Conservative 62; Mismatches 178; Indels 63; Gaps 13;

Qy	73	IGTCFSTASLKQWRSVSMFPTRLSPCSSATQTERDSATAYRMTVEVLGTVLGTAIQOI	132
Db	119	LGLCYSLVNIPIYGLSATAMTQQ--PQSRARLGAARGAAS--LTFVCLAFILGPSIK---	171
Qy	133	VGQADTPCFQDFNSSTVASQSANHTGTTSHRETQKAYLLAAGVIVCIYIICAVILILGV	192

Db 111 MTRYAYYSIGAGLVAAVYQVSWCLAAAGROIHKIRKQFFHAIMRQEIQWDFVDHVG 170
 Qy 211 RGLRLV-----MSHGPKIKLITGFLTSLAFMLVEGNFVLCFTYTLGFRNEFQNLAIM 265
 Db 171 LNRLTDDVKINEGIDKI--GMFFQSM-----TEFTGFIIVGFTRGWKLTLVILA 220
 Qy 266 LSAT--LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL-----304
 Db 221 ISPLGLSAVAKWILSSFTDKELLAYAKAGAAVEVLAIRIVIAFGGOKKELERYKN 280
 Qy 305 MESNLIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFY-----359
 Db 281 LLEAKRIGIKAITANISIGAAFLLIYASVAVF-----WYGTTLVLSGEYSIGQV 331
 Qy 360 --VFFTKFASVSGISGLTSLDF-----AGYQ-----TRGCSOPERVKFT 397
 Db 332 LTVEFSLVIGAFSGVQASPSIEAFANARGAAEYEFKIIDNKPSIDSYSKSGHKPDNIK--389
 Qy 398 LNMLVTMAPIVLILGLLLEK-----MYPIDEERRONKKALQALRDEASS-----S 444
 Db 390 -----GNLEFRNVHFSYP-----SRKEVKILKGLNLKQVSGQTVALVGN 429
 Qy 445 GCSETDSTEL 454
 Db 430 CGCKSTTVQL 439

RESULT 9
 US-09-316-167-2
 ; Sequence 2, Application US/09316167
 ; Patent No. 6365357
 ; GENERAL INFORMATION:
 ; APPLICANT: Mechetter, Eugene
 ; APPLICANT: Roninson, Igor B
 ; TITLE OF INVENTION: Methods and Reagents for Preparing and
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boenhen Hulbert & Berghoff Ltd.
 ; STREET: 300 South Wacker Drive, Seventh Floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/316,167
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/752,447
 ; FILING DATE: 15-NOV-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6365357nan, Kevin E
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 95,1121
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-9808
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1280 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-316-167-2

Query Match 4.5%; Score 107.5; DB 4; Length 1280;
 Best Local Similarity 19.5%; Pred. No. 0.27;

Matches 84; Conservative 67; Mismatches 148; Indels 131; Gaps 19;
 Qy 115 MTEVGLTVL---GTAIQGIVGQ-----ADTPCFQDFNSSTVASQSANHTGTTSHRE- 165
 Db 51 MMYGTAAIIHAGLPLMLLVFGEMTDIFANAGNLEDLMNITNRSINDTGFPMNLEED 110
 Qy 166 -TOKAYL---LAAGVIVICIVICAVILILGVRE---OREPYEAQQSEPIAYF-----210
 Db 111 MTRYAYYSIGAGLVAAVYQVSWCLAAAGROIHKIRKQFFHAIMRQEIQWDFVDHVG 170
 Qy 211 RGLRLV-----MSHGPKIKLITGFLTSLAFMLVEGNFVLCFTYTLGFRNEFQNLAIM 265
 Db 171 LNRLTDDVKINEGIDKI--GMFFQSM-----TEFTGFIIVGFTRGWKLTLVILA 220
 Qy 266 LSAT--LTIPIWQWFLTRFGKKTAVYVGISSAVPFLILVAL-----304
 Db 221 ISPLGLSAVAKWILSSFTDKELLAYAKAGAAVEVLAIRIVIAFGGOKKELERYKN 280
 Qy 305 MESNLIITYAVAAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFY-----359
 Db 281 LLEAKRIGIKAITANISIGAAFLLIYASVAVF-----WYGTTLVLSGEYSIGQV 331
 Qy 360 --VFFTKFASVSGISGLTSLDF-----AGYQ-----TRGCSOPERVKFT 397
 Db 332 LTVEFSLVIGAFSGVQASPSIEAFANARGAAEYEFKIIDNKPSIDSYSKSGHKPDNIK--389
 Qy 398 LNMLVTMAPIVLILGLLLEK-----MYPIDEERRONKKALQALRDEASS-----S 444
 Db 390 -----GNLEFRNVHFSYP-----SRKEVKILKGLNLKQVSGQTVALVGN 429
 Qy 445 GCSETDSTEL 454
 Db 430 CGCKSTTVQL 439

RESULT 10
 5268463-8
 ; Patent No. 5268463
 ; APPLICANT: JEFFERSON, RICHARD A.
 ; TITLE OF INVENTION: PLAAAT PROMOTER a-GLUCURONIDASE GENE
 ; CONSTRUCT
 ; NUMBER OF SEQUENCES: 9
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/447,976
 ; FILING DATE: 08-DEC-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 119,102
 ; FILING DATE: 10-NOV-1987
 ; APPLICATION NUMBER: 264,586
 ; FILING DATE: 31-OCT-1988
 ; SEQ ID NO: 8:
 ; LENGTH: 426
 ; 5268463-8

Query Match 4.5%; Score 107; DB 6; Length 426;
 Best Local Similarity 19.0%; Pred. No. 0.059;
 Matches 71; Conservative 59; Mismatches 169; Indels 74; Gaps 14;
 Qy 73 IGTCFSTIASLKQWSRVSMFPTRLSPCSSATQETPRDSATAYMTVEVLTGVLTAIOGQI 132
 Db 111 LGLCYSLVNIPIYGSLATAMTQQ--PQSRARLGAARGIAAS--LTFVCLAFILGPSIK---163
 Qy 133 VQADTPCFQDFNSSTVASQSANHTGTTSHRETKAYLLAAGVIVICIVICAVILILGV 192
 Db 164 -----NSSPEEMVSVYH-----FWTIVLATAGWV--LYFTIC-----FKST 196
 Qy 193 REQREPYEAQQSEPIAYFRLGLRLVMSHGPKIKLITGFLTSLAFMLVEGNFVLCFTYTLG 252
 Db 197 RENVRIVAPSLNIS---LQTLKRRNPLFMLCIGALCVLISTFAVSASLFF---YVLN 249
 Qy 253 FRNEFQNLAIMLSATLTIPIW-----QWFLTRFGKKTAVYVGISSAVPFLILVAL 304
 Db 250 DTGLFTVLVL-----VQNPGWYCGIGTAGAXMVARIGKTKFLIGALLGTCGYLLFPFW 302

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	2384	100.0	458	9	US-09-999-598-20		Sequence 20, Appl
2	2384	100.0	458	9	US-09-989-293A-20		Sequence 20, Appl
3	2384	100.0	458	9	US-09-989-735-20		Sequence 20, Appl
4	2384	100.0	458	9	US-09-990-444-20		Sequence 20, Appl
5	2384	100.0	458	9	US-09-989-730-20		Sequence 20, Appl
6	2384	100.0	458	9	US-09-990-436-20		Sequence 20, Appl
7	2384	100.0	458	9	US-09-991-181-20		Sequence 20, Appl
8	2384	100.0	458	9	US-09-993-687-20		Sequence 20, Appl
9	2384	100.0	458	9	US-09-989-734-20		Sequence 20, Appl
10	2384	100.0	458	9	US-09-997-653-20		Sequence 20, Appl
11	2384	100.0	458	9	US-09-993-667-20		Sequence 20, Appl
12	2384	100.0	458	9	US-09-990-438-20		Sequence 20, Appl
13	2384	100.0	458	9	US-09-990-562-20		Sequence 20, Appl
14	2384	100.0	458	9	US-09-997-428-20		Sequence 20, Appl
15	2384	100.0	458	9	US-09-997-666-20		Sequence 20, Appl
16	2384	100.0	458	9	US-09-990-711-20		Sequence 20, Appl
17	2384	100.0	458	9	US-09-989-726-20		Sequence 20, Appl
18	2384	100.0	458	9	US-09-990-437-20		Sequence 20, Appl
19	2384	100.0	458	9	US-09-998-156-20		Sequence 20, Appl

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: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/09178
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091962
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 2384; DB 9; Length 458;

Query Match	100.00;	Score	2.504;	DB 3;	Length	456;	
Best Local Similarity	100.00;	Pred. No.	5.4e-185;				
Matches	458;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;

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61	QY	61	S	G	S	C	P	T	S	H	A	R	I	P	G	T	C	F	S	I	A	S	L	K	O	W	S	M	F	P	T	R	L	S	P	C	S	S	A	T	E	O	T	E	R	D	S	A	T	A	R	M	T	V	E	L	120	
61	Db	61	S	G	S	C	P	T	S	H	A	R	I	P	G	T	C	F	S	I	A	S	L	K	O	W	S	M	F	P	T	R	L	S	P	C	S	S	A	T	E	O	T	E	R	D	S	A	T	A	R	M	T	V	E	L	120	
121	QY	121	G	T	V	L	G	T	A	I	O	G	I	V	G	A	D	T	P	C	F	D	E	N	S	T	V	A	S	Q	S	A	N	H	T	G	T	S	H	R	E	T	Q	K	A	Y	L	L	A	A	G	V	I	C	I	180		
121	Db	121	G	T	V	L	G	T	A	I	O	G	I	V	G	A	D	T	P	C	F	D	E	N	S	T	V	A	S	Q	S	A	N	H	T	G	T	S	H	R	E	T	Q	K	A	Y	L	L	A	A	G	V	I	C	I	180		
181	QY	181	Y	I	C	A	V	I	L	L	G	R	Q	R	E	P	E	Y	A	Q	O	S	E	P	T	A	Y	R	G	L	R	L	N	S	H	G	P	Y	I	K	L	I	T	G	F	L	T	S	L	A	E	M	V	E	240			
181	Db	181	Y	I	C	A	V	I	L	L	G	R	Q	R	E	P	E	Y	A	Q	O	S	E	P	T	A	Y	R	G	L	R	L	N	S	H	G	P	Y	I	K	L	I	T	G	F	L	T	S	L	A	E	M	V	E	240			
241	QY	241	G	N	F	V	L	C	T	Y	T	L	G	R	N	E	F	O	N	L	L	A	I	M	L	S	A	T	I	P	I	W	Q	F	L	T	R	F	C	K	T	A	V	Y	G	I	S	S	A	P	P	F	L	I	300			
241	Db	241	G	N	F	V	L	C	T	Y	T	L	G	R	N	E	F	O	N	L	L	A	I	M	L	S	A	T	I	P	I	W	Q	F	L	T	R	F	C	K	T	A	V	Y	G	I	S	S	A	P	P	F	L	I	300			
301	QY	301	L	V	A	L	M	E	S	N	L	I	T	Y	A	V	A	A	G	I	S	V	A	A	F	L	L	P	W	S	M	L	P	D	V	I	D	D	F	H	L	K	Q	P	H	F	H	G	T	E	P	I	F	S	F	V	360	
301	Db	301	L	V	A	L	M	E	S	N	L	I	T	Y	A	V	A	A	G	I	S	V	A	A	F	L	L	P	W	S	M	L	P	D	V	I	D	D	F	H	L	K	Q	P	H	F	H	G	T	E	P	I	F	S	F	V	360	
361	QY	361	F	F	T	F	A	S	G	V	S	L	G	I	S	T	L	S	D	F	A	G	Y	T	R	C	S	O	P	E	R	V	K	F	T	L	N	M	L	M	T	A	P	I	V	L	L	I	L	L	L	L	L	L	L	L	L	420
361	Db	361	F	F	T	F	A	S	G	V	S	L	G	I	S	T	L	S	D	F	A	G	Y	T	R	C	S	O	P	E	R	V	K	F	T																							

RESULT 2

US-09-989-293A-20
; Sequence 20, Application US/09989293A
; Patent No. US20020177164A1

GENERAL INFORMATION:

APPLICANT:	Askenazi, Avi J.
APPLICANT:	Baker, Kevin P.
APPLICANT:	Botstein, David
APPLICANT:	Desnoyers, Luc
APPLICANT:	Eaton, Dan L.
APPLICANT:	Ferrara, Napoleone
APPLICANT:	Fong, Sherman
APPLICANT:	Gerber, Hanspeter
APPLICANT:	Gerritsen, Mary E.
APPLICANT:	Goddard, Audrey
APPLICANT:	Godowski, Paul J.
APPLICANT:	Grimaldi, J. Christopher
APPLICANT:	Gurney, Austin L.
APPLICANT:	Kijavini, Ivar J.
APPLICANT:	Napier, Mary A.
APPLICANT:	Pad, James

RESULT 3

US-09-989-735-20
: Sequence 20, Application US/09989735
: Publication No. US20020193299A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C61
: CURRENT FILING DATE: 2001-11-19
: CURRENT APPLICATION NUMBER: US/09/989,735
: PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2384; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.4e-185;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MMLRWALSPPSSCLMAEPCMPQTPWASASANPPGPANVALPCGSSSPRPWPSLPTSS 60
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Qy 61 SGSCPTSHTRPCTGCTCFISIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYMTVEVL 120
Db 61 SGSCPTSHTRPCTGCTCFISIASLKQWSRVSMFPTRLSPCSSATEQTERDSATAYMTVEVL 120
Qy 121 GTVLGTAIQGOIVGOADTPCFQDFNSSTVASQSANHTGTTSHRETOKAYLLAAGVIVCI 180
Db 121 GTVLGTAIQGOIVGOADTPCFQDFNSSTVASQSANHTGTTSHRETOKAYLLAAGVIVCI 180
Qy 181 YIICAVILILGVREQREPEYEAQOSEPTAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVE 240
Db 181 YIICAVILILGVREQREPEYEAQOSEPTAYFRGLRLVMSHGPYIKLITGFLFTSLAFMLVE 240
Qy 241 GNEVLFCTYTLGFRNEFQNLILAISATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI 300
Db 241 GNEVLFCTYTLGFRNEFQNLILAISATLTIPIWQWFLTRFGKKTAVYVGISSAVPFLI 300
Qy 301 LVALMESNLITTYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360
Db 301 LVALMESNLITTYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360
Qy 361 FFTKFAAGSVLSIGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPITVLILGLLFLPKMY 420
Db 361 FFTKFAAGSVLSIGISTLSLDFAGYQTRGCSQPERVKFTLNMLVTMAPITVLILGLLFLPKMY 420
Qy 421 PIDEERRRQNKALQALRDEASSSGCSETSTELASIL 458
Db 421 PIDEERRRQNKALQALRDEASSSGCSETSTELASIL 458

RESULT 6
US-09-990-436-20
; Sequence 20, Application US/09990436
; Publication No. US20020198148A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.

;; PRIOR APPLICATION NUMBER: 60/090445
;; PRIOR FILING DATE: 1998-06-24
;; PRIOR APPLICATION NUMBER: 60/090472
;; PRIOR FILING DATE: 1998-06-24
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;; PRIOR FILING DATE: 1998-07-02
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;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2384; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.4e-185;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLRWALSPSSCLWAPGHPQSQTPTWASASANPPGPAWVALCPGSSPPRPWLSPTSS 60
Db 1 MRLRWALSPSSCLWAPGHPQSQTPTWASASANPPGPAWVALCPGSSPPRPWLSPTSS 60
Qy 61 SGSCPTSHARPICGTFCFASLKQWSRVSMPTRLSPCSSATEQTERDSATAYRTMVEVL 120
Db 61 SGSCPTSHARPICGTFCFASLKQWSRVSMPTRLSPCSSATEQTERDSATAYRTMVEVL 120
Qy 121 GTVLGTAIQGQIVGQADTPCQDFNSSTVASQSANHTTGTTSHTRETOKAYLLAAGVIVCI 180
Db 121 GTVLGTAIQGQIVGQADTPCQDFNSSTVASQSANHTTGTTSHTRETOKAYLLAAGVIVCI 180
Qy 181 YIICAVILILGVREQREYEAQQSEPIAYFRGLRLVMSHGHIYIKLITGFLTSLAFMLVE 240
Db 181 YIICAVILILGVREQREYEAQQSEPIAYFRGLRLVMSHGHIYIKLITGFLTSLAFMLVE 240
Qy 241 GNEVLFCTYTGFRNEFONLLAILMSATLPIWQWFLTRFGKKTAVYVGISSAVPPLI 300
Db 241 GNEVLFCTYTGFRNEFONLLAILMSATLPIWQWFLTRFGKKTAVYVGISSAVPPLI 300
Qy 301 LVALMESNLIITYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKOPFHGTEPIFFSFYV 360
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Qy 361 FFTKFAVSGLISTLSLDFAGYQTRGCSQPERVKFTLNMLVTWAPIVLIILGLLKKMY 420
Db 361 FFTKFAVSGLISTLSLDFAGYQTRGCSQPERVKFTLNMLVTWAPIVLIILGLLKKMY 420
Qy 421 PIDERRRQNKALQALRDEASSSGCSETDSTELASIL 458
Db 421 PIDERRRQNKALQALRDEASSSGCSETDSTELASIL 458

RESULT 7

US-09-991-181-20
; Sequence 20, Application US/09991181
; Publication No. US20020197615A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tamas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730PIC53
;; CURRENT APPLICATION NUMBER: US/09/991.181
;; CURRENT FILING DATE: 2001-11-16
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
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US-09-993-687-20
; Sequence 20, Application US/09993687
; Publication No. US20020198149A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Gerritsen, Mary E.
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; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC11
; CURRENT APPLICATION NUMBER: US/09/993,687
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APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC64
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR FILING DATE: 60/049787
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?	PRIOR FILING DATE:	1998-07-07
?	PRIOR APPLICATION NUMBER:	60/092182
?	PRIOR FILING DATE:	1998-07-09

Qy	1	MWLWALSIPPSCLWAEPGMPSTPWWASANPPGPAAWVLCPCGSSSRPRMPSLPTSS	60
Dd	1	MWLWALSIPPSCLWAEPGMPSTPWWASANPPGPAAWVLCPCGSSSRPRMPSLPTSS	60
Qy	61	SGSCPTSHTRPIGTGCFSIASKOWSRVSMPETRLSPCSSSATEQTERDSATAYRMVFEVL	120
Dd	61	SGSCPTSHTRPIGTGCFSIASKOWSRVSMPETRLSPCSSSATEQTERDSATAYRMVFEVL	120
Qy	121	GTVLGTAIQGIIVGOADTPCTFOFNSTSVASOSANHHTGTTTSHRETKAYLLAAGVIVCI	180
Dd	121	GTVLGTAIQGIIVGOADTPCTFOFNSTSVASOSANHHTGTTTSHRETKAYLLAAGVIVCI	180

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 2384; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.4e-185;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MWLRWALSPPSSCLWAEPGMPQSOTPWMAASASANPPGPAWVALCPGSSSPRPWPSLPTSS 60
DB      1 MWLRWALSPPSSCLWAEPGMPQSOTPWMAASASANPPGPAWVALCPGSSSPRPWPSLPTSS 60

QY      61 SGSCPTSHTPARPTGTCFSTASLKQMSRVSMFPTRLSPCSSATQTERDSATAYRMTVEVL 120
DB      61 SGSCPTSHTPARPTGTCFSTASLKQMSRVSMFPTRLSPCSSATQTERDSATAYRMTVEVL 120

QY      121 GTVLGTAIQGQIVGQADTPCFQDFNSSTVASGSANTHGTGTTSHRETQKAYLLAAGVIVCI 180
DB      121 GTVLGTAIQGQIVGQADTPCFQDFNSSTVASGSANTHGTGTTSHRETQKAYLLAAGVIVCI 180

QY      181 YIICAVILILGVREQREPEYAQOSEPIAYFRGLRLVMSHGPIYIKLTIGLFTSLAPMLVE 240
DB      181 YIICAVILILGVREQREPEYAQOSEPIAYFRGLRLVMSHGPIYIKLTIGLFTSLAPMLVE 240

QY      241 GNFVLCTYTLGFRNEFQNLALLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAYVPFLI 300
DB      241 GNFVLCTYTLGFRNEFQNLALLAIMLSATLTIPIQWFLTRFGKKTAVYVGISSAYVPFLI 300

QY      301 LVALMESNLIIITYAVAAVAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360
DB      301 LVALMESNLIIITYAVAAVAGISVAAAFLLPWSMLPDVIDDFHLKQPHFGHTEPIFFSFYV 360

QY      361 FTTKFAAGSYLGISTLSLDFAGYQTRGCCQOPERVKFTLNMLVTMAPITVLILGLLLFKMY 420
DB      361 FTTKFAAGSYLGISTLSLDFAGYQTRGCCQOPERVKFTLNMLVTMAPITVLILGLLLFKMY 420

QY      421 PIDEERRRKNKALQALRDEASSGCGSETDSTELASIL 458
DB      421 PIDEERRRKNKALQALRDEASSGCGSETDSTELASIL 458

RESULT 12
US-09-990-438-20
; Sequence 20, Application US/09990438
; Publication No. US20030027754A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; APPLICANT: Zheng, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

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; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 2384; DB 9; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.4e-185;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MWLRWALSPPSSCLWAEPMSQTPWASASANPPGPAWALPCGSSSPRPWPSLPTSS 60
Db 1 MWLRWALSPPSSCLWAEPMSQTPWASASANPPGPAWALPCGSSSPRPWPSLPTSS 60
Qy 61 SGSCPTSHTRPITGTCFSTASLKQWSRVSMFPTRLSPCSSATQTERDSATAYRMTVEVL 120
Db 61 SGSCPTSHTRPITGTCFSTASLKQWSRVSMFPTRLSPCSSATQTERDSATAYRMTVEVL 120
Qy 121 GTVLGTAGIOIGVQADTCFQDFNSTVASQSANHTGTTSHRETKAYLLAAGVIVCI 180
Db 121 GTVLGTAGIOIGVQADTCFQDFNSTVASQSANHTGTTSHRETKAYLLAAGVIVCI 180
Qy 181 YIICAVILLGVREQREPEAQOSEPIAYFRGLRLVMSHGPYIKLITGFLTSLAPMLVE 240
Db 181 YIICAVILLGVREQREPEAQOSEPIAYFRGLRLVMSHGPYIKLITGFLTSLAPMLVE 240
Qy 241 GNEVLFCTYTLGRNFEFQNLALLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAYPFLI 300
Db 241 GNEVLFCTYTLGRNFEFQNLALLAIMLSATLTIPIWQWFLTRFGKKTAVYVGISSAYPFLI 300
Qy 301 LVALMESNLIIITYAVAVAAGISVAIAFLLPWSMLPDVIDDFHLKQPHFHGTEPIFFSFYV 360
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Qy 361 FFTKFAAGSVGLSTLSLDFAGYQTRGCCQPERVKFTLNMVTPMIPVILILLGLLFKMY 420
Db 361 FFTKFAAGSVGLSTLSLDFAGYQTRGCCQPERVKFTLNMVTPMIPVILILLGLLFKMY 420
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Db 421 PIDERRRQNKALQALRDEASSGCGSETDSTELASIL 458
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RESULT 13

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US-09-990-562-20
; Sequence 20, Application US/09990562
; Publication No. US20030027985A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: F2730PIC18
; CURRENT APPLICATION NUMBER: US/09/990,562
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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US-09-997-428-20
Sequence 20, Application US/09997428
Publication No. US20030027162A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C44
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:44:36 ; Search time 15 Seconds
(without alignments)
1266.411 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MRLRWALSLPPSSCLWAEFG.....DEASSGCGSETDSTELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	221.5	9.3	544	1 YD74_SYNY3	P74168 synechocyst
2	153.5	6.4	463	1 GUTA_BACSU	O34368 bacillus su
3	146	6.1	479	1 XVL_P_LACPE	P67992 lactobacill
4	143.5	6.0	457	1 UDB_ECOLI	P30868 escherichia
5	138.5	5.8	459	1 YMB_BACSU	O34961 bacillus su
6	138	5.8	641	1 RAPP_PEDPE	P43466 pediococcus
7	133	5.6	463	1 YNAJ_BACSU	P94488 bacillus su
8	131.5	5.5	438	1 SHIA_ECOLI	P76350 escherichia
9	126.5	5.3	460	1 YAGG_ECOLI	P75683 escherichia
10	125	5.2	462	1 LACP_STAXY	O33814 staphylococ
11	112	4.7	272	1 YCR3_ERWHE	Q01334 erwinia her
12	110	4.6	485	1 YIHO_ECOLI	P32136 escherichia
13	110	4.6	1780	1 POLG_MVEV	P05769 m genome po
14	109.5	4.6	422	1 EXUT_BACSU	O34456 bacillus su
15	109	4.6	457	1 BAG4_HUMAN	O95429 homo sapien
16	106.5	4.5	1280	1 MDR1_HUMAN	P08183 homo sapien
17	106	4.4	408	1 GPT_HUMAN	Q9h3h5 homo sapien
18	106	4.4	580	1 UAPC_EMENI	P48777 americella
19	105.5	4.4	512	1 MYIN_BORBU	O51750 borrelia bu
20	105	4.4	473	1 YIHO_SALTY	Q19174 salmonella
21	101.5	4.3	605	1 YIHO_YEAST	P38739 saccharomyc
22	101	4.2	476	1 MELB_SALTY	P30878 salmonella
23	101	4.2	830	1 VPP3_HUMAN	Q13488 h vacuolar
24	101	4.2	1887	1 REBL_DROME	P04052 drosophila
25	100.5	4.2	653	1 CMWF_RHOCA	Q00500 rhodobacter
26	100.5	4.2	1367	1 AMYH_YEAST	P08640 saccharomyc
27	100	4.2	415	1 CSCB_ECOLI	P30000 escherichia
28	99	4.2	408	1 GPT_CRIGR	P24140 cricetus
29	99	4.2	410	1 GPT_MOUSE	P42867 mus musculu
30	99	4.2	567	1 PROI_LETEN	P13865 leishmania
31	98.5	4.1	284	1 CDX4_HUMAN	O14627 homo sapien
32	98.5	4.1	428	1 YXIO_BACSU	P42306 bacillus su
33	98.5	4.1	452	1 WZYE_SALTY	P37458 salmonella

RESULT 1									
ID	YD74_SYNY3								
AC	P74168;								
DT	15-DEC-1998 (Rel. 37, Created)								
DT	15-DEC-1998 (Rel. 37, Last sequence update)								
DT	16-OCT-2001 (Rel. 40, Last annotation update)								
DE	Hypothetical symporter sl11374.								
GN	SL11374.								
OS	Synechocystis sp. (strain PCC 6803).								
OC	Bacteria; Cyanobacteria; Chroococcales; Synechocystis.								
OX	NCBI_Taxid=1148;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=97061201; PubMed=8905231;								
RA	Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,								
RA	Miyajima N., Hirotsawa M., Sugiyama M., Sasamoto S., Kimura T.,								
RA	Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,								
RA	Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,								
RA	Tabata S.;								
RT	"Sequence analysis of the genome of the unicellular cyanobacterium								
RT	Synechocystis sp. strain PCC6803. II. Sequence determination of the								
RT	entire genome and assignment of potential protein-coding regions.";								
RL	DNA Res. 3:109-136(1996).								
CC	- - SUBCELLULAR LOCATION: Integral membrane protein (Potential).								
CC	- - SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY								
CC	(SGF).								
CC	-----								
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CC	use by non-profit institutions as long as its content is in no way								
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/								
CC	or send an email to license@isb-sib.ch).								
CC	-----								
DR	EMBL; D90912; BAA18257.1; -								
DR	InterPro; IPR001927; Na/Gal_symp.								
DR	TIGRfam; TIGR00792; gph; 1.								
DR	PROSITE; PS00872; NA_GALACTOSIDE_SYMP; FALSE_NEG.								
KW	Hypothetical protein; Transport; Transmembrane; Symport;								
KW	Complete proteome.								
FT	TRANSMEM 31	51							
FT	TRANSMEM 52	72							
FT	TRANSMEM 84	104							
FT	TRANSMEM 116	136							
FT	TRANSMEM 162	182							
FT	TRANSMEM 191	211							
FT	TRANSMEM 230	250							
FT	TRANSMEM 257	277							
FT	TRANSMEM 318	338							
FT	TRANSMEM 356	376							
FT	TRANSMEM 383	403							
FT	TRANSMEM 407	427							
FT	TRANSMEM 450	470							
FT	TRANSMEM 501	521							

P23338 cricetus
P92669 macropus ro
O82396 salmonella
P38387 mycobacteri
Q9mzt2 oryctolagus
P21448 cricetus
P76037 escherichia
P52067 escherichia
Q48624 leuconostoc
P43245 rattus norv
Q92633 homo sapien
Q928j6 chlamydia p

ALIGNMENTS

YD74_SYNY3
ID YD74_SYNY3 STANDARD; PRT; 544 AA.

AC P74168;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical symporter sl11374.
GN SL11374.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

OX NCBI_Taxid=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirotsawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. II. Sequence determination of the
entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).

CC -|- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -|- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
(SGF).

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CC EMBL; D90912; BAA18257.1; -
DR InterPro; IPR001927; Na/Gal_symp.
DR TIGRfam; TIGR00792; gph; 1.
DR PROSITE; PS00872; NA_GALACTOSIDE_SYMP; FALSE_NEG.
KW Hypothetical protein; Transport; Transmembrane; Symport;

Complete proteome.
FT TRANSMEM 31 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 84 104 POTENTIAL.
FT TRANSMEM 116 136 POTENTIAL.
FT TRANSMEM 162 182 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 230 250 POTENTIAL.
FT TRANSMEM 257 277 POTENTIAL.
FT TRANSMEM 318 338 POTENTIAL.
FT TRANSMEM 356 376 POTENTIAL.
FT TRANSMEM 383 403 POTENTIAL.
FT TRANSMEM 407 427 POTENTIAL.
FT TRANSMEM 450 470 POTENTIAL.
FT TRANSMEM 501 521 POTENTIAL.

```

Db 339 FIMFASGFTTPLNTLAWGVADCDVDAEWKT-----GIRADGVWISSMSFINKGLVALA 394
Qy 371 LGISTSLDAGYQTRGCSQPERVKFTLNMLVTMAPIV---LILLGLLLEKMYPIDER 426
Db 395 GSFSAYILGAGY-----VANTDQTVASNAIKNNALIPGFFILLISILLIAFTPLTEKR 449

RESULT 3
ID XYLP_LACPE STANDARD; PRT; 479 AA.
AC P96792;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Putative xylose-proton symporter (xylose transporter).
GN XYLP.
OS Lactobacillus pentosus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1589;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MD353;
RA MEDLINE=98233724; PubMed=9573180;
RA Chaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W.,
RA Pouwels P.H.;
RT "Cloning, sequence analysis, and characterization of the genes
RT involved in isoprimeverose metabolism in Lactobacillus pentosus.";
RL J. Bacteriol. 180:2312-2320(1998).
RN [2]
RP REVISIONS.
RA Chaillou S., Lokman B.C., Leer R.J., Posthuma C., Postma P.W.,
RA Pouwels P.H.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RESPONSIBLE FOR TRANSPORT OF XYLOSE INTO THE CELL, WITH
CC THE CONCOMITANT EXPORT OF A PROTON (SYMPORT SYSTEM).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
CC (SGF).
CC -----
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CC -----
CC EMBL; U89276; AAC62250.1; -
CC InterPro; IPR001927; Na/Gal_symp.
CC Pfam; PF00083; sugar_tr: 1.
CC TIGRFAMs; TIGR00792; gph; 1.
CC PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
KW TRANSMEM 54 74
FT TRANSPORT; Sugar transport; Transmembrane; Symport.
FT TRANSMEM 54 74
FT TRANSMEM 102 122
FT TRANSMEM 131 151
FT TRANSMEM 174 194
FT TRANSMEM 205 225
FT TRANSMEM 253 273
FT TRANSMEM 289 309
FT TRANSMEM 321 341
FT TRANSMEM 348 368
FT TRANSMEM 397 417
FT TRANSMEM 431 451
SQ SEQUENCE 479 AA; 52505 MW; 1555AD1084D459C7 CRC64;

Query Match 6.18; Score 146; DB 1; Length 479;
Best Local Similarity 20.98; Pred. No. 0.0042;
Matches 85; Conservative 68; Mismatches 157; Indels 96; Gaps 18;
Qy 76 CFSIASLQK-----WSRSVMFTPLRSLPCSSATEQTERDSATAYRTMVE 118

```

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Db 118 CFTVPMNSTGKVVWVAYVTYIGVDVLYSAVNIPITSILPSLTSNPQE-----RYTSL 169
Qy 119 VLGTVLGTATOGITGOADTPCQODENSSIVASOSANHTGTTSHRETQKAYLLAAGVIV 178
Db 170 TIRQFMGT-LGATITSTIALPLVAYFGGSGTSS-----AHG-----WFVVALIMA 213
Qy 179 CIIYICAVILILGVREQREPEYEAQOSEPIAFYFGRGLRVLVMSHGPPYIKLITGFLTSLAFML 238
Db 214 VIAWIFFIVFANTKERVQVQSKSIPIK--TSLKALKRNPWPWVVI--FI----- 261
Qy 239 VEGNVLFCTYTTLGRNEFO-----NULLAIMLSAYLTPIPIWQWFTTRF 282
Db 262 ---NFI---YWLGMQTRSQVTYFFKYNMHDATLASFILGLQVALLAVVITPTWTKARI 314
Qy 283 GKKTAVYVGISSA-VPELILVALMESLIITYAVAAAGISVAAAF--LPWSMLPDVID 339
Db 315 GKRTMLMGLLAIVGQLILWGGSKALNVPTITVTIGVY-LGTGFVSGLIAMLAUSDV 373
Qy 340 DFHLKQPHFGH--TEPIFFSFYVFFTFASGVSLGISTLSLDFAGYQTRGCSQPERVKFT 397
Db 374 YGEWK-----NGVRAEGIVTSFSSFAKFGMGIGGAVTGLILSAGYVYVHANHAQSAQALN-A 428
Qy 398 LNMVLTMAPIV---LILLGLLLEKMYPI-----DEERRONKKAL 434
Db 429 IEMNVVWPIVGFGLSIAILLFYKVDKIEPKMLADLEQKHAQENAL 474

RESULT 4
ID UIDB_ECOLI STANDARD; PRT; 457 AA.
AC P30868; P77457;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glucuronide carrier protein (glucuronide permease).
GN UIDB OR GUSB OR UIDP OR Bi616.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RA Jefferson R.A.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RN Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RC MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubraman S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RN DNA Res. 3:363-377(1996).
RN [4]
RP PRELIMINARY SEQUENCE OF 1-112 FROM N.A.
RX MEDLINE=87041472; PubMed=3534890;
RA Jefferson R.A., Burgess S.M., Hirsh D.;

```

KW Hypothetical protein; Transport; Transmembrane; Symport;
KW Complete proteome.

FT TRANSMEM 25 45 POTENTIAL.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 95 115 POTENTIAL.
FT TRANSMEM 123 143 POTENTIAL.
FT TRANSMEM 167 187 POTENTIAL.
FT TRANSMEM 192 212 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 279 299 POTENTIAL.
FT TRANSMEM 310 330 POTENTIAL.
FT TRANSMEM 332 352 POTENTIAL.
FT TRANSMEM 389 409 POTENTIAL.
FT TRANSMEM 420 440 POTENTIAL.
SQ SEQUENCE 459 AA; 50420 MW; B807795C3276E1E3 CRC64;

Query Match 5.88; Score 138.5; DB 1; Length 459;
Best Local Similarity 18.98; Pred. No. 0.013;
Matches 63; Conservative 70; Mismatches 167; Indels 33; Gaps 8;

QY 99 SSATEOPE-RDSATAYRMVTEVLGTGLTALQGVQADTPCFQDFNSSTVASQSANHT 157
DB 149 AAMTQSEDTSTSTFRQ-TGSGALFITSV-----AVMPLLVKEDNPKV----- 192
QY 158 HGTSTHRETOKAYLLAAGVIVCIYICAVILILGVREOREPEYEAQOQSEIAYFRGLRVM 217
DB 193 -----GYPVVMGLFAALGVFWFYCYRNCKEKRIIIEAPK-EKLTLSVVKTFI 240
QY 218 SHGPYIKLNGFTLSTAFMLVEGNFVLCFTYILGFNRFQNLALLMLSATLTIPTWQW 277
DB 241 TNKPLTLVLMTIFSTISAYNIKSAMLYFAQYNLGNVELMAYMNFIIIGSFLGVVFLPK 300
QY 278 FLTRFGKKTAVYVIGSISAVPFLILVALMESNLITYAVAAAGISVAAAFLLPMSLPDV 337
DB 301 LVKMFGRKRTAMGFGISVADLINFMLPSNVVFTILASIAFISGIPNGIWTALVSDI 360
QY 338 IDDFHLKOPHGHTEPIFFSYVFFTFKASGVSLGISTLSLDFAGYQTRGCSQPERVKFT 397
DB 361 IDYGEWKSQ--ERKEATTYSLEFNFSRKLQSLGSLGIGLIGY-VPNAVQTAQALIG 417
QY 398 LNMIVTMAPIVLILGLLLPK-MYPTDEERRQ 429
DB 418 IKALLLPALALAMFIIGFLYKLTDDQHAQ 450

RESULT 6

ID RAPPPEDPE STANDARD; PRT; 641 AA.
AC P43466;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Raffinose carrier protein (Raffinose permease).
GN RAFF.
OS Pedicoccus pentosaceus.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Pedicococcus.
OX NCBI_TaxID=1255;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PPPE.0;
RA Leenhouts K.K.J., Bolhuis A.A., Kok J.J., Venema G.G.;
RL Submitted (XXX-1994) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: IN THE N-TERMINAL SECTION: BELONGS TO THE
CC SODIUM: GALACTOSIDE SYMPORTER FAMILY (SGF).
CC -!- SIMILARITY: CONTAINS 1 PTS EIIA DOMAIN.

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DR EMBL; Z32771; CA83664.1; -;
DR EMBL; L32093; AA25563.1; -;
DR HSP; P20166; IGPR.
DR InterPro; IPR001927; Na/Gal_symp.
DR InterPro; IPR001127; PTS_EIIA.
DR Pfam; PF00358; PTS_EIIA.1; 1.
DR ProDom; PD002243; PTS_EIIA.1.
DR TIGRFAMS; TIGR00792; Gph; 1.
DR TIGRFAMS; TIGR00830; PBA; 1.
DR PROSITE; PS00371; PTS_EIIA.1; 1.
DR PROSITE; PS00872; NA_GALACTOSIDE_SYMP; 1.
KW Transmembrane; Sugar transport; Transport; Symport; Phosphorylation.
FT DOMAIN 1 ? SGF DOMAIN.
FT DOMAIN ? 641 EIIA DOMAIN.
FT MOD_RES 559 559 PHOSPHORYLATION (BY HPR) (BY SIMILARITY).
FT TRANSMEM 25 45 POTENTIAL.
FT TRANSMEM 57 77 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 168 188 POTENTIAL.
FT TRANSMEM 201 221 POTENTIAL.
FT TRANSMEM 253 273 POTENTIAL.
FT TRANSMEM 288 308 POTENTIAL.
FT TRANSMEM 317 337 POTENTIAL.
FT TRANSMEM 342 362 POTENTIAL.
FT TRANSMEM 394 414 POTENTIAL.
FT TRANSMEM 429 449 POTENTIAL.
FT TRANSMEM 485 505 POTENTIAL.
SQ SEQUENCE 641 AA; 69913 MW; 15BEC5F69F8C0F61 CRC64;

Query Match 5.88; Score 138; DB 1; Length 641;

Best Local Similarity 19.88; Pred. No. 0.021;

Matches 73; Conservative 61; Mismatches 168; Indels 66; Gaps 13;

QY 77 FSIASLKWQSRVSMFPTRLSPCSSATEQTERDSATAYRMVTEVLGTGLTALQGVQQA 136
DB 138 YSPKDVGFW---SMLP-----SLTDSREREKTATFAR-----LGSTIGGLVGLV 180
QY 137 DTPCFQDFNSSTVASQSANHTGTTSHRETKAYLLAAGVIVCIYICAVILI-----L 190
DB 181 VMPAVIFFSAKATS-----TGDN-----GMFIFALIIICLIASANGVGL 221
QY 191 GVREOREPEYEAQOQSEIAYFRGLRVMSHGSPYIKLTGFTLSTAFMLVEGNFVLCFTY 250
DB 222 GTREVDSDIRKNKQDVTGVMEIFKALAKNDOLLAAALAYLEYGVGINLSLEVYFTYI 281
QY 251 LGFRNEFQ-----NLLLAIMLSATLTIPIWOMFLTRFGKKTAVYVIGSISAVPFLI---L 301
DB 282 MGRPKSPSILSIINIFGLI--ATSLFPV-----LSKKFSRKGVPAG--CLVFMGGIAI 332
QY 302 VALMESNLITYAVAAAGISVAAAFLLPMSLPDVDDHFKLQPHGHTEPIFFSFYVF 361
DB 333 FTIAGSNLWLVLLAATMFGFPQMVFLVLMVITDSVEYQGLKLG--HRDESLSLSVRPL 390
QY 362 FTKFASGVSLG-----ISTLSLDFAGYQTRGCSQPERVKFTLNMIVTMAPIVLILGLLL 417
DB 391 IDKFGGAINGVVQCIALISGTTGTATASSITAAGQLHFKLTMPAFPALMLIIAIGIPSK 450
QY 418 KMPIDEE 425
DB 451 QIFLTEEK 458

RESULT 7

ID YNAJ_BACSU STANDARD; PRT; 463 AA.
AC P94488;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE Hypothetical symporter ynaJ.

```
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
RA Saito N., Sempel G., Seki Y., Sivasubramaniam S., Tagami H.,
RA Takeda J., Takenoto K., Wada C., Yamamoto Y., Horiuchi T.,
RA "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE SUGAR TRANSPORTER FAMILY.
CC
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CC
CC EMBL; U88529; AAC46271.1; -.
CC EMBL; AE000250; AAC75045.1; -.
CC EMBL; D90837; BAA13801.1; -.
CC EcoGene; EG20205; shiA.
CC InterPro; IPR004736; Cit_H_symport.
CC InterPro; IPR003662; sub_transporter.
CC Pfam; PF00083; sugar_tr.1.
CC TIGRFAMs; TIGR00883; 2A0106; 1.
CC PROSITE; PS00216; SUGAR_TRANSPORT_1; FALSE_NEG.
CC PROSITE; PS00217; SUGAR_TRANSPORT_2; 1.
CC Transport; Transmembrane; Inner membrane; Symport; Complete proteome.
CC
CC DOMAIN 1 27
CC TRANSMEM 28 48
CC DOMAIN 49 63
CC TRANSMEM 64 84
CC DOMAIN 85 108
CC TRANSMEM 109 129
CC DOMAIN 130 132
CC TRANSMEM 133 153
CC DOMAIN 154 167
CC TRANSMEM 168 188
CC DOMAIN 189 192
CC TRANSMEM 193 213
CC DOMAIN 214 254
CC TRANSMEM 255 275
CC DOMAIN 276 286
CC TRANSMEM 287 307
CC DOMAIN 308 317
CC TRANSMEM 318 337
CC DOMAIN 338 340
CC TRANSMEM 341 363
CC DOMAIN 364 386
CC TRANSMEM 387 407
CC DOMAIN 408 410
CC TRANSMEM 411 431
CC DOMAIN 432 438
CC CYTOPLASMIC (POTENTIAL).
CC SEQUENCE 438 AA; 47817 MW; B7FEBD5AFDAE8CC CRC64;..
CC
CC Query Match 5.58; Score 131.5; DB 1; Length 438;
CC Best Local Similarity 22.38; Pred. No. 0.038;
CC Matches 78; Conservative 56; Mismatches 121; Indels 95; Gaps 18;
CC
CC 127 AIOGQIVGQADTPCFDFNSSTVAS-OSANTHTGTTSHRETKAY----LAAAGVVICIY 181
CC ||||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC 133 AIOGFVAG-----GEMGGALLSVESAPKNKAFYSSGVQVGVGLLSTGLVSLIS 185
CC ||||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC 182 I-----ICAVILILG---VR-----EQREPEYAAQSQEPYAFRGL 213
CC : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC 186 MMTTDEQFLSGWRIPFLFSIVLVGALWVRNGMESAEFEQOQHOAAKKRIPVIEAL 245
CC : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC 214 RLVMNH-GPYIKLTGFLTSLAFMLVEGNEVLCFTYTLGRN-FOPLLAIIMLSATLT 271
CC : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC 246 ---LRHPGAFKIIIALRICELLTWYIVTAFALNYSQNMGLPRELFLNIGLVGGLSCLT 302
CC : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
CC
CC 272 IPIQWFLTRGKK---TAVYGVSSAVPEPILVALMESNLITTYAVAAISVAAAF 327
CC ||| : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
CC 303 IPCFAWLADRGRRRVITGLTGLTSLAFPEFMALDAQSIWVFFSI----- 350
CC ||| : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
CC 328 LLPWSMLPDVIDDF--HLKOPHFHGTETIFFSFVFFTKFASGVSGLSTLSLDPAGYQT 385
CC ||| : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
CC 351 -----MLANIAHDMVVCQOPMF--TE-MFCASYRY-----SGAGVGQVAVVGGGF-- 395
CC ||| : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
CC 386 RGCSQPERVKTLNMLVTM-----APIVLILGLLGLLKKMYPY----DEER 426
CC ||| : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
CC 396 -----TPPIAALITYFAGNMHSVAIYLLAGCLISAMTALLMKDSQR 437
CC ||| : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : : ||| : :
CC
CC RESULT 9
CC YAGG_ECOLI STANDARD; PRT; 460 AA.
CC AC YAGG_ECOLI AC YAGG_ECOLI AC YAGG_ECOLI AC YAGG_ECOLI AC YAGG_ECOLI
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40; Last annotation update)
CC DE Hypothetical symporter yagG.
CC GN YAGG OR B0270.
CC OS Escherichia coli.
CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Escherichia.
CC OX NCBI_TaxID=562;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=K12 / MG1655;
CC RX MEDLINE=97426617; PubMed=9278503;
CC RA Blatter F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
CC Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
CC Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
CC Mau B., Shao Y.;
CC RT "The complete genome sequence of Escherichia coli K-12.";
CC RL Science 277:1453-1474(1997).
CC RN [2]
CC RP SEQUENCE FROM N.A.
CC RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
CC Davis K., Federpiet N., Hyman R., Kaiman S., Komp C., Kurdi O.,
CC Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
CC Davis R.W.;
CC RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
CC (SGF). STRONG, TO E.COLI YICJ.
CC
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CC
CC EMBL; AE000135; AAC73373.1; -.
CC EMBL; U70214; AAB08691.1; -.
CC EcoGene; EGI3346; yagG.
CC InterPro; IPR001927; Na/Gal_sym.
CC TIGRFAMs; TIGR00792; gph; 1.
CC PROSITE; PS00872; NA_GALACTOSIDE_SYM; 1.
CC KW Hypothetical protein; Transport; Transmembrane; Inner membrane;
CC Symport; Complete proteome.
CC FT TRANSMEM 10 30 POTENTIAL.
CC FT TRANSMEM 31 51 POTENTIAL.
CC FT TRANSMEM 79 99 POTENTIAL.
CC FT TRANSMEM 107 127 POTENTIAL.
CC FT TRANSMEM 151 171 POTENTIAL.
CC FT TRANSMEM 180 200 POTENTIAL.
CC FT TRANSMEM 263 283 POTENTIAL.
CC FT TRANSMEM 309 329 POTENTIAL.
```

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CC -----
DR EMBL: M87280; AAA64975.1; -
DR InterPro: IPR001927; Na/Gal_symp.
DR PROSITE: PS00872; NA_GALACTOSIDE_SYMP; FALSE_NEG.
KW Hypothetical protein.
SQ SEQUENCE 272 AA; 29955 MW; C7C753B416F14AB6 CRC64;

Query Match 4.7%; Score 112; DB 1; Length 272;
Best Local Similarity 22.88; Pred. No. 0.5;
Matches 67; Conservative 41; Mismatches 122; Indels 64; Gaps 12;
QY 167 QKAYLLAAGVIVCIYICAV-----ILILGVREQREPEYEAQQSEPIAYFGRGLRVMHSG 220
Db 17 QHRWLCLEFGV---AYIFSVNGGLTQTLILG-----QLLRWHA 51
QY 221 PYKILITGFTSLAPMLVE--GNFVLFCTYITIGRNEFONLLATMLSLTPIPIWQWF 278
Db 52 PPSTLTLYMLATLPQFISYLGAMFYVYIYLGSAFYFMWLAHILKRAAGSLAKRL 111
QY 279 LTRFGK-----KQAVYVGISSAVPF-----LILVALMESNLITTVAVAVAAGISVAAAF 327
Db 112 TRFNKVQIFCYCAVLGVLISIALFPAPKSVFVLVPL-----TFIISTL-----YQATT 160
QY 328 LLPWSMLPDVIDDFHLKQPHFGTEPIFFSYFFFTKFAAGVSLGISTLSLDLAFGYOTRG 387
Db 161 TLMWVMADVADYGENSQG--KRMDDGIIFSTFLAVLKLGNALSGAIVGWLFGSYV--- 215
QY 388 CSQPERVKFNLMLVTHAPIVILLGLLFF---KMPIDERRRQ--NKKALQAL 437
Db 216 ANAPEQTSAMHCIVALFTVYVPGLLSLAFAFATLRWYKLDQTMQEIINLAKMQTI 269

RESULT 12

-YIHO_ECOLI
ID YIHO_ECOLI STANDARD; PRT; 485 AA.
AC P32136; P76774;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical symporter YIHO.
GN YIHO OR B3876.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RC MEDLINE=93347969; PubMed=8346018;
RA Plunkett G. III, Burland V.D., Daniels D.L., Blattner F.R.;
RA "Analysis of the Escherichia coli genome. III. DNA sequence of the
RT region from 87.2 to 89.2 minutes."
RL Nucleic Acids Res. 21:3391-3398(1993).
RN [2]
RP REVISIONS.
RC STRAIN=K12 / MG1655;
RC MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE SODIUM:GALACTOSIDE SYMPORTER FAMILY
CC (SGF).
CC -----

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CC -----
DR EMBL: LJ9201; AAB03009.1; ALT_FRAME.
DR EMBL: AE00463; AAC76873.1; ALT_INIT.
DR PIR: S40820; S40820.
DR EcoGene: EGI1841; yiho.
DR InterPro: IPR001927; Na/Gal_symp.
DR TIGRams: TIGR00792; gph; 1.
DR PROSITE: PS00872; NA_GALACTOSIDE_SYMP; 1.
KW Hypothetical protein; Transport; Transmembrane; Inner membrane;
KW Symport; Complete proteome.
FT TRANSMEM 17 37 POTENTIAL.
FT TRANSMEM 54 74 POTENTIAL.
FT TRANSMEM 88 108 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
FT TRANSMEM 185 205 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 275 295 POTENTIAL.
FT TRANSMEM 303 323 POTENTIAL.
FT TRANSMEM 325 345 POTENTIAL.
FT TRANSMEM 379 399 POTENTIAL.
FT TRANSMEM 414 434 POTENTIAL.
SQ SEQUENCE 485 AA; 53817 MW; FB53C0CE17756500 CRC64;

Query Match 4.68; Score 110; DB 1; Length 485;
Best Local Similarity 20.78; Pred. No. 1.3;
Matches 82; Conservative 54; Mismatches 172; Indels 88; Gaps 15;
QY 72 PIGTCFSA-----SLKQSRVSMFETRLSPCSATEQTERDSATAYRMTVEVLGT 122
Db 113 PVKTTATALFMFMFGLSYSLMNCYGAIP-----AITKNPNERAQLAAYRQGGATIGL 166
QY 123 VLGTATOGQIVGQADTPCFQDFNSSTVASANHTGTTSHRETQKAYLLAAGVIVCIYI 182
Db 167 LICTV-----AFIPLQSLFSDSTVGYACA-----ALMFSIGGF----- 199
QY 183 ICAVILILGVREQREPEY--EAQOSEPIAYFGRGLRVMHSGPIYKILITGFTSLAPMLVE 240
Db 200 ---IFMMLCYRGVKEHYVDTPPTGHKASILKSCAIFRNPLLVLCIANLCTLAFAFIKL 256
QY 241 GNFLVFTYTLGFRNEFONLL-----LAIMLSATLTIPIWQWFLRFRGKKTAVYVIGIS 293
Db 257 AIQVYTYQYVL---NDI-NLLSWMGFFSMCGILIGLVLLVPL---TVKCFGKKQYVLAGMV 309
QY 294 SAVPFLILVALMESNLITTVAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHFG--- 350
Db 310 LWAVGVDILNVFWGNSFTFVNFSCVAFGTAFVNSLNWALVPTVD-----YGEWK 360
QY 351 ----TEPIFFSYFFFTKFAAGVSLGISTLSLDLAFGYOTRGCSQPERVKFTLNMLVTPMAP 406
Db 361 TGTRAEGSVTYGTFFFRKISAAALAGFLPGIMLTQIGY-VPNIAQSDATLOGROLIFITWP 419
QY 407 IVL-ILGLLLLFKMPIDEEER-----RRONKK 432
Db 420 CALAIIAALTMGFFYTLNEKRFALLIEINQKNKE 455

RESULT 13

POLG_MVEV
ID POLG_MVEV STANDARD; PRT; 1780 AA.
AC P05769;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Genome polyprotein [Contains: Capsid protein C (Core protein); Matrix
DE protein (Envelope protein M); Major envelope protein E; Nonstructural
DE proteins NS1, NS2A, and NS2B; Protease/helicase (EC 3.4.21.98) (NS3)]
DE (Fragment).
OS Murray valley encephalitis virus.

SEQUENCE FROM N.A.
 STRAIN=168;
 MEDLINE=98240225; PubMed=9579062;
 RA Rivolta C., Soldo B., Lazarevic V., Joris B., Maue C., Karamata D.;
 RT "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
 containing a putative 12.3 kb operon involved in hexuronate catabolism
 element.";
 RT and a perfectly symmetrical hypothetical catabolite-responsive
 element.";
 RL Microbiology 144:877-884(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Avevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Guiseppi G., Guy B.J., Haga K., Haeleth J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullio M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Perrean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: ALDOHEXURONATE TRANSPORT SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE PHTHALATE PERMEASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF015825; AAC46332.1; .
 DR EMBL; 299110; CAB13093.1; .
 DR Subtilist; BG13210; exuT.
 DR InterPro; IPR004744; Gal_transport.
 DR InterPro; IPR003662; sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 DR TIGRfams; TIGR00893; 2A0114; 1.
 KW Transmembrane; Transport; Complete proteome.
 FT TRANSMEM 9 29 POTENTIAL.
 FT TRANSMEM 45 65 POTENTIAL.
 FT TRANSMEM 82 102 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 163 183 POTENTIAL.
 FT TRANSMEM 219 239 POTENTIAL.
 FT TRANSMEM 256 276 POTENTIAL.
 FT TRANSMEM 294 314 POTENTIAL.
 FT TRANSMEM 321 341 POTENTIAL.

FT TRANSMEM 356 376 POTENTIAL.
 FT TRANSMEM 381 401 POTENTIAL.
 SQ SEQUENCE 422 AA; 45313 MW; C2E291AF347F7EDD CRC64;
 Query Match 4.68; Score 109.5; DB 1; Length 422;
 Best Local Similarity 21.9%; Pred. No. 1.2;
 Matches 88; Conservative 58; Mismatches 133; Indels 123; Gaps 19;
 QY 62 GSCPTSHTRPCTGCTCFASLAKQWSRVSMPEPTL-----SPCSSATEQ-----TER 107
 DB 71 GAKLTLEVMVWVSLFSGAVALAFGFSVLLIIRILFCMGEGPLSATINKVNNWFPPTQR 130
 QY 108 DSATAYRMTVEVLGTGTGTAIOGIVGQADTPCFQDFNSSTVASQSANHTGTTSHRETQ 167
 DB 131 ASV-----IGVNTSGTGLGASGPIVGM-----AVAF----- 159
 QY 168 KAYLLAAGVIVCIYIICAVILILGVREOREPYEAQOSEPAYFRGLRVLMVSHGP----- 221
 DB 160 -SWKVSFVLIIMIGLIWAVLWFKVKE--KPQETIKRAP-----AIKAETSPGKEIPLTF 211
 QY 222 YIKLITGFLFTSLAFMLVEGNEFVLCFTYITLGFNREFONILL-----AIMLSATLTIPIWQWF 278
 DB 212 YLAQKT-VLETAFAFAY--NYILFF-----FLTWPSYLVDERGLSVESMSYITVIPWI 263
 QY 279 LTRFG-----KKTAVYGVGISSAVPFILILVALMESNLIITVA--VAVAA----- 320
 DB 264 LGFGLAAGGFGVSDDYVYKKA-RKGVLSRKVVLVTLFSSAVLIGFAGLVATTAGAVTL 322
 QY 321 ISVAAAF-----LPWSMLPDVDDHFKQPHFGHETPIFFSFVFFTKFASGVSIGIST 375
 DB 323 VALSVFLYLTGAIYNAVIVQDVVDQNV-----GSVGGFMHFLA----- 361
 QY 376 LSLDFAGYQTRGCSQSPERVKFTNMLVLTAPIVLILGLLLF 417
 DB 362 -----NTAGIIGPALTGFIYDQGTGFGAFLAGGLAVF 395
 RESULT 15
 BAG4_HUMAN
 ID BAG4_HUMAN STANDARD; PRT; 457 AA.
 AC O95429; O95818;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE BAG-family molecular chaperone regulator-4 (Silencer of death
 DE domains).
 GN BAG4 OR SODD
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99091615; PubMed=9873016;
 RA Takayama S., Xie Z., Reed J.C.;
 RT "An evolutionarily conserved family of Hsp70/Hsc70 molecular
 RT chaperone regulators.";
 RL J. Biol. Chem. 274:781-786(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99115917; PubMed=9915703;
 RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
 RT "Prevention of constitutive TNF receptor 1 signaling by silencer of
 RT death domains.";
 RL Science 283:543-546(1999).
 RN [3]
 RP ERRATUM.
 RA Jiang Y., Woronicz J.D., Liu W., Goeddel D.V.;
 RL Science 283:1852-1852(1999).
 CC -1- FUNCTION: INHIBITS THE CHAPERONE ACTIVITY OF HSP70/HSC70 BY
 CC PROMOTING SUBSTRATE RELEASE.
 CC -1- SUBUNIT: BINDS TO THE ATPASE DOMAIN OF HSP70/HSC CHAPERONES.
 CC -1- SIMILARITY: CONTAINS 1 BAG DOMAIN.

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OM protein - protein search, using sw model

Run on: June 19, 2003, 17:45:42 ; Search time 19 Seconds
(without alignments)
2317.346 Million cell updates/sec

Title: US-09-941-992-20

Perfect score: 2384

Sequence: 1 MWLRWALSPPSSCLWAEFG.....DEASSGGCSTDELASIL 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	308.5	12.9	487	2 AB2269	hypothetical prote
2	221.5	9.3	544	2 S75696	melibiose carrier
3	154	6.5	445	2 E97320	sugar, proton sympo
4	153.5	6.4	463	2 H69788	H+-symporter homol
5	147	6.2	514	2 H87465	sodium-galactoside
6	145	6.1	449	2 D96985	permease of the Na
7	144.5	6.1	457	2 C90919	glucuronide permaa
8	144.5	6.1	457	2 H85767	glucuronide permaa
9	143.5	6.0	457	2 B64918	glucuronide permaa
10	138.5	5.8	459	2 D69852	sodium/galactoside
11	138	5.8	641	2 S44253	raffinose carrier
12	133	5.6	463	2 A69888	H+-symporter homol
13	132.5	5.6	477	2 AC0122	Sodium,galactoside
14	131.5	5.5	438	2 G64962	shikimate transport
15	128.5	5.4	438	2 H85822	probable transport
16	127.5	5.3	438	2 B90976	shikimate transport
17	127.5	5.3	466	2 B91186	probable permaase
18	127.5	5.3	466	2 A86033	probable permaase
19	126.5	5.3	460	2 F64752	probable melibiose
20	126	5.3	463	2 D87624	sodium-galactoside
21	119	5.0	490	2 B86813	xyloside transport
22	118	4.9	458	2 B97324	sugar/Na+(H+) simp
23	117.5	4.9	1136	2 C75483	probable drug tran
24	113	4.7	457	2 AE0507	probable transport
25	113	4.7	467	2 F91228	probable permaase
26	112	4.7	272	2 S52977	hypothetical prote
27	112	4.7	317	2 S53316	mucin (clone PGM-2
28	112	4.7	469	2 E86075	probable permaase
29	112	4.7	541	2 D82302	iron(III) ABC tran

RESULT 1

AB2269

hypothetical protein alr3705 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp.

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002

C:Accession: AB2269

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AB2269

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-487 <KUR>

A:Cross-references: GB:BA000019; PIDN:BA075404.1; PID:g17132839; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: alr3705

Query Match 12.9%; Score 308.5; DB 2; Length 487;

Best Local Similarity 25.5%; Pred. No. 1e-15;

Matches 92; Conservative 68; Mismatches 148; Indels 53; Gaps 10;

QY 93 TRLSPPSSATEQTERDSATAYRMTVEVLGTVLCTAQOIVGQADPCQDFNSSTVASQ 152

DB 151 TALTP-ELTQDYDERTSLNSFRFAFSIGGSILSLIL-----SKVLSL 192

QY 153 SANHTGTTSHRETOKAYLLAGVIVICIVICAVILVGVREOREPEYA-----QOSEPI 207

DB 193 IS-----DRQQYIVLAICTVIVISILYWCVGVREVRVLAFAKRIQVESDSI 242

QY 208 AYFRGLRLVMSHGPIKLTIGTFLTSLFALMVEGNVFLFTYTYTLGF-RNEFQNLALLAML 266

DB 243 PFEQQLKIVFSNRPFVIGVLFSLMGVQITASIIPYFVINCMSPESDPTTMAVQG 302

QY 267 SATLTTPIQWFLTRFGKKTAVYVGISSAVPFLIIVA----LMESNLIITYAVAAAGIS 322

DB 303 TALLMLFVWTALSKKIGKLVFLMGSS---WIIAAGLFFLPQGGIGLMYNAIMAGVG 359

QY 323 VAAAFLLPWSMLPDVI--DDFHLKOPHFHGTETPFISFYVFFKFGASVSLGSLTSLDF 380

DB 360 VSTAYLVPMSPMDVDIELDELQTCQRR-----EGIFGFWVLQKFGALFGLVGNALQA 415

QY 381 AGY-----QTRGCSQPERVKFTLNMLVTMAPITVLILGLLLFKMYPIDERRRQNKAL 434

DB 416 SGFKEAVAGQTTLPIQPESALFAIRAVGPLPTICILFGLVLYFYFYPITREMHAEILLKL 475

QY 435 Q 435

DB 476 Q 476

hypothetical prote
tetracycline resis
probable permaase
genome polyprotein
hexuronate transp
cation efflux syst
tetracycline resis
gastric mucin (clo
cathionc amino aci
hypothetical prote
transport system p
hypothetical prote
probable amino aci
hypothetical prote
multidrug resistan
transport system p

A:Gene: rafp
C:Superfamily: phosphotransferase system glucose-specific enzyme II, factor III homolog
C:Keywords: sugar transport; transmembrane protein
F:485-639/Domain: phosphotransferase system glucose-specific enzyme II, factor III homolog

Query Match 5.8%; Score 138; DB 2; Length 641;
Best Local Similarity 19.8%; Pred. No. 0.01;
Matches 73; Conservative 61; Mismatches 168; Indels 66; Gaps 13;

QY 77 FSIASLKQWSRVSMFTRLSPSCSSATEQTERDSATAYRMTVEVLGTGLTAIGQIVGQA 136
DB 138 YSFKDVGFV---SMLP-----SLTTDSRERKTATFAR-----LGSITGGGLVGL 180
QY 137 DTPCFODFNSTVASOSANHTGTTTSHRETQKAYLLAAGVIVCIYIICAVILI-----L 190
DB 181 VMPAVIFFSAKATS-----TGDN-----GWFIALICILIALISAMGVGL 221
QY 191 GYVREQREPYEAQOSEPIAYFRGLRLVNSHGPIKLTIGLFTSLAFMLVEGNEFLCTVT 250
DB 222 GTREVDSDIRKNQDVTGVWEIFKALAKNDQLLWAAALYLFYGVGINLGSLEVYFTYI 281
QY 251 LGRNRFQ-----NLLLAIMLSATLPIPIWQMFTRFGKKTAYVVGISSAVPPLI----L 301
DB 282 MGKPKSFSILSTINIFGLI--ATSLFPV-----LSKKFSRKGKGFAG---CLVFMGLGIAL 332
QY 302 VALMESNLITTYAVAVAAGISVAAAFLLPWSMLPDVIDDFHLKQPHGHGTEPIFFSYVF 361
DB 333 FTIAGSNLMLVLLAATMFGPQOMVFLVWLWITDSVEYQOLKLG--HRDESLSLSVRPL 390
QY 362 FYKFAAGVSLG----ISTLSLDFAGVQTRGCCSOPERVKTLNLMVTMAPIVLLIGLLLF 417
DB 391 IDKFGAISNGVVGQIAIISGMTTGTATASSITAAAGLHFKLTMFAFPALMLLIAIGFSK 450
QY 418 KMPYIDEE 425
DB 451 QIFLTEEK 458

RESULT 12
A:Accession: A69888
H+-symporter homolog ynaJ - Bacillus subtilis
C:Species: Bacillus subtilis
C:date: 03-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: A69888
R:Kunst, S.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Broutelle, S.; Bruchli, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.;
Koetter, P.; Konlingstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scani
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69888
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-463 <KUN>
A:Cross-references: GB:299113; GB:AL009126; NID:g26334090; PIDN:CAB13641.1; PID:g26341
A:Experimental source: strain 168
C:Genetics:
A:Gene: ynaJ
C:Superfamily: melibiose carrier protein

Query Match 5.6%; Score 133; DB 2; Length 463;
Best Local Similarity 22.8%; Pred. No. 0.01;
Matches 84; Conservative 65; Mismatches 138; Indels 82; Gaps 21;

```
Qy 272 IPIWQFLTRFGKK-----TAVYVGISSAVPFLILVALMESNLITITAVAVAGISVAAAF 327
Db 303 IPCFAWLADRGRRRVYITGLTGLSAFFFFMALEAQSIFFWIVFFSI----- 350
Qy 328 LLQWSMLPDVIDDF--HLKQPHFHGTEPIFFSFYVFTKFSAGVSLGISTLSLDFAGYQT 385
Db 351 -----MLANTAHDMVVCQQPMF--TE-MEGASYRY-----SGAGVGYQVASVVXGCF-- 395
Qy 386 RGCSPQPRVFTLNMLVTM-----APIVLILGLLLFKMYPi---DEER 426
Db 396 -----TPFIAAALITYFAGNWHSVAIYLLAGCLISAMTALIMKDSQR 437

RESULT 15
H85822
probable transport protein, shikimate shiA [imported] - Escherichia coli (strain O157:H7)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: H85822
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85822
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-438 <STO>
A:Cross-references: GB:AE0051174; NID:g12516157; PIDN:AAG57044.1; GSPDB:GN00145; UWGP:231
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: shiA
C:Superfamily: citrate utilization determinant

Query Match 5.4%; Score 128.5; DB 2; Length 438;
Best Local Similarity 21.6%; Pred. No. 0.035;
Matches 75; Conservative 58; Mismatches 125; Indels 89; Gaps 17;

Qy 127 AIQGOIYGQADTFQDFDNSTVAS-QSANHTGCTTSHRETOKAY-----LLAAGVIVCIY 181
Db 133 AIQGFVAG-----GEWGAALLSVESAPKPKKAFYSSGVQGVYGVGLLSTGLSVLS 185
Qy 182 I-----ICAVILILGV-----REQREPYEAQOSEPIAYFRGLRLV--- 216
Db 186 MMTTDEQFLSWGRIPLFSIVLVGALWVRNGMEESAEEFQQYQNOAAKKRIPVIEAL 245
Qy 217 MSH-GPIYKILITGLFTSLAPMLVEGNFVLCFTYTLGRNE-FONLLLAIMLSATLPIPI 274
Db 246 LRHPGAFKIIALRCCELLTMYIVTAFALNYSQNMGLPRELFLNIGLLVGLSCLTIPC 305
Qy 275 WQWFLTRFGKK---TAVYVGISSAVPFLILVALMESNLITITAVAVAGISVAAAFLLP 330
Db 306 FAWXADRGRRRVYITGALIGTUSAFFFFMALEAQSIFFWIVFFSI----- 350
Qy 331 WSMPLPDVIDDF--HLKQPHFHGTEPIFFSFYVFTKFSAGVSLGISTLSLDFAGYQTRGC 388
Db 351 --MLANTAHDMVVCQQPMF--TE-MEGASYRY-----SGAGVGYQVASVVXGCF----- 395
Qy 389 SQPRVFTLNMLVTM-----APIVLILGLLLFKMYPi---DEER 426
Db 396 -----TPFIAAALITYFAGNWHSVAIYLLAGCLISAMTALIMKDNQR 437
```

Search completed: June 19, 2003, 17:48:26
Job time : 22 secs

Result No.	Query			DB	ID	Description
	Match	Length	Score			
1	76.2	530	1816	4	Q96F59	Q96F59 homo sapien
2	75.8	371	1807	4	Q9BRC8	Q9BRC8 homo sapien
3	65.3	534	1556.5	11	Q8DA75	Q8DA75 mus musculus
4	12.9	487	308.5	16	Q8YQV7	Q8YQV7 anabaena sp
5	7.1	455	169.5	16	Q8RR83	Q8RR83 thermoanaer
6	7.0	463	168	16	Q8XP13	Q8XP13 clostridium
7	6.5	445	154	16	Q97DQ0	Q97DQ0 clostridium
8	6.2	514	147	16	Q9A7H5	Q9A7H5 caulobacter
9	6.1	449	145	16	Q97L68	Q97L68 clostridium
10	6.1	454	144.5	16	Q8XMC0	Q8XMC0 clostridium
11	6.1	457	144.5	16	Q8X673	Q8X673 escherichia
12	6.0	652	142	2	Q93807	Q93807 lactobacilli
13	5.6	477	132.5	16	Q8ZHA9	Q8ZHA9 yersinia pe
14	5.5	444	131.5	16	Q8ZKR3	Q8ZKR3 salmonella
15	5.3	438	127.5	16	Q8X4U5	Q8X4U5 escherichia
16	5.3	466	127.5	16	Q8XDK7	Q8XDK7 escherichia

Db 372 VFPLILVALMERNLIVTVVAAGVSAAFLPNSMLPDVDDFHLKHPHSPGTEPIF 431
QY 356 FSFYVFFTKFASGVSLGISTLSLDFAGYQTRGCSQPERVAFKTLNMLVTMAPIVLILGLL 415
Db 432 FSFYVFFTKFASGVSLGISTLSLDFANFYQRCSCQPEQVFTLKMVVTMAPIVLILGLL 491
QY 416 LFKMTPIDERRRQNKALQALRDSEASSGSGSETDSTELASIL 458
Db 492 LFKLYPIDEKRRQNKALQALREASSGSGSDTSTELASIL 534
RESULT 4
Q8YQV7
ID Q8YQV7 PRELIMINARY; PRT; 487 AA.
AC Q8YQV7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypochemical protein Alr3705.
DE ALR3705.
GN ANabaena sp. (strain PCC 7120).
OS Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL: AF003594; BAB/5404.1; -;
DR InterPro: IPR001927; Na/Gal_symp.
DR TIGRFAMs: TIGR00792; gph; 1.
KW Hypochemical protein; Complete proteome.
SQ SEQUENCE 487 AA; 54313 MW; 5C52801DC071A47E CRC64;
Query Match 12.9%; Score 308.5; DB 16; Length 487;
Best Local Similarity 25.5%; Pred. No. 3.3e-16;
Matches 92; Conservative 68; Mismatches 148; Indels 53; Gaps 10
QY 93 TRLSPCSSATEGTERDSATAYRMVTEVLGTVLGTAIQGIQVQADTPCFODFNSSTVASQ 152
Db 151 TALTP-ELTQDTEFSLNSRFFAFSGTSLIL-----SKVLSL 192
QY 153 SANHTGTTSHRETOKAYLLAAGVICVITICAVILIGLVREQPEYEA-----QOSEPI 207
Db 193 IS-----DRQQYIVLAAICTVISLSLWCVGVRVLAFAEKRIQVESDSI 242
QY 208 AYFGRGLRVMSHGPIKILITGLFTSLAFMLVEGNFVLFTCTYILGF-RNPFQMLLAIML 266
Db 243 PFPEQLKIVFSNRPLFVIGILFSLWGLVQITASIPIFYVINCMSLPSESDVPTMTAVQ 302
QY 267 SATLTIPTIOWELTFRGKKTAVYVGISSAVPEFLILVA---LMESNLIITYAVAAAGIS 322
Db 303 TALLMLFWMTALSKGIGKGLVFLGMS--WIATAAGLFFLPQGIGLMYMAVAGV 359
QY 323 VAAAFLLPWSMLPDVI--DDFHLKQPHFGHTEPIFFSYVFFTKFASGVSLGISTLSLDF 380
Db 360 VSTAVLPWSMIPDVIELDELQTORR-----EGIFYGFVLLQKFLGFLVLGNALQA 415
QY 381 AGY-----QTRGCSQPERVFTLNMVVTMAPIVLILGLLFLKMWPIDERRQNKAL 434
Db 416 SGFKEAVAGQTTLPIQPESALFAIRAVGPLPTICLIFGLVLTIFYFYPITREHAEILLKL 475
QY 435 Q 435
Db 476 Q 476

```
QY 146 SSTVASOSANHTGTTSHRETQKAY--LLAAGVIVCIYIIC-----184
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 169 SIVVLSQTANGAVLSSDYQORSRVYGMWQAANVGMVILVCLPPFITGVKGDHDSVRA 228
| | | | | : : : : | | | | | : : : |
QY 185 -----AVIILGVREOREPEYEAQOSEPIAYFGRGLRVMSHGPYKILITGFLFTSLA 235
| | | | | : : : : | | | | | : : : |
Db 229 MGNFVILLPTITVLLAVMTVKEPAAPQHGKTGLKQYWRLLMR--PSVQRL--LFADLL 283
| | | | | : : : : | | | | | : : : |
QY 236 FMLVEG---NFVLFCTYTLGF--RNEFQNLALLAMLSATLTIPWQWFLTRFGKKTAVYV 290
| | | | | : : : : | | | | | : : : |
Db 284 MGLAPGAGTGLFLFFFERIKGFDKTOAGVULLVYFLAALAGAPLWMLAKKLGKHKALVV 343
| | | | | : : : : | | | | | : : : |
QY 291 GISSAVPFLIL----VALMESNLIIITYAVAAAGISVAAAFLLPWSMLPDVIDDHFHLKQP 346
| | | | | : : : : | | | | | : : : |
Db 344 ---AAVYAFVQVCAVMPAGSSVMGMLLVLAGLPYSAPVLRVSRMADIGDEERLES- 399
| | | | | : : : : | | | | | : : : |
QY 347 HFHGTEDIFFSVFFTKFASGVSLSGIST--LSLDFAGYQTRGCSQPERVFTLNMLVTMA 405
| | | | | : : : : | | | | | : : : |
Db 400 ---GVDKTGLLYAIVTGTVKLGYALAVAFIALGWMGFDPK-VSTPEGDAALIGM-YAIA 454
| | | | | : : : : | | | | | : : : |
QY 406 PIVILILGLLLFKMYPIDEERRQNKALQALRDEA---SSSGCSETDS 451
| | | | | : : : : | | | | | : : : |
Db 455 PAALGLVAAIMRMRYPLDRLAEIQRL--AARDAAAADASKSAPSDDS 502
| | | | | : : : : | | | | | : : : |
```

RESULT 9

```
Q97L68
ID Q97L68 PRELIMINARY; PRT; 449 AA.
AC Q97L68;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Permease of the Na+ galactoside symporter family.
GN CAC0694.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R.L., Lee H.M., Dubois J., Qiu D., Hatti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007584; AAK78671.1; -
DR InterPro; IPR001927; Na/Gal_symp.
DR TIGRFAMS; TIGR00792; gph; 1.
KW Complete proteome.
SQ SEQUENCE 449 AA; 49887 MW; B447E0CF70C2C997 CRC64;
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Query Match 6.1%; Score 145; DB 16; Length 449;
Best Local Similarity 23.2%; Pred. No. 0.0022;
Matches 63; Conservative 49; Mismatches 128; Indels 32; Gaps 9;

QY 170 YLLAAGVIVCIYIICAVILILGVREOREPEYEAQOSEPIAYFGRGLRVMSHGPYKILITGF 229
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 179 YPVVAGTGLIGILSFYMTKYKTRVVAPAENVKKEITPKSTAVTFTNRLALLTLTLMT 238
| | | | | : : : : | | | | | : : : |
QY 230 -LFTSLAPMLVGNFVLECTYTLGFRNEFQNLALLAMLS-----ATLTIPWQWFLTRFG 283
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 239 IFSISAYNIRSSIVYVCOYNLG-----NVTLLPYINFTIGCAVLGVSFMPKLVGRFG 292
| | | | | : : : : | | | | | : : : |
QY 284 KKTAVYGVGISSAVPFLILVALMESNLII-----TYAVAAAG-ISVAAAFLLPWSMLPDV 337
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 293 KKRTAIG-----FLISVTAADSNIFLPGNIVITFTLLAIGFISIPNGITWAFVSDS 346
| | | | | : : : : | | | | | : : : |
QY 338 IDDFHLKQPHFGT--EPIFFSFYVFTKTFASGVSLSGISTLSLDFAGYQTRGCSQPERVK 395
| | | | | : : : : | | | | | : : : |
```

```
Db 347 IDYGEWRT---GTRREGITYSVENFARKLAQSTAGLLSGMGLGFVGY-VANKQSAHAL 401
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
QY 396 FTNLNMLYMAP-IVLILGLLLFKMYPIDEER 426
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 402 FGKALLMAYPAVALLVAALTIIGLLYNLSDKK 433
| | | | | : : : : | | | | | : : : |
```

RESULT 10

```
Q8XMC0
ID Q8XMC0 PRELIMINARY; PRT; 454 AA.
AC Q8XMC0;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable sugar transport protein.
GN GUTA OR CPE0769.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003188; BAB80475.1; -
DR InterPro; IPR001927; Na/Gal_symp.
DR TIGRFAMS; TIGR00792; gph; 1.
KW Sugar transport; Complete proteome.
SQ SEQUENCE 454 AA; 49661 MW; 9EDB58F22755A90E CRC64;
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Query Match 6.1%; Score 144.5; DB 16; Length 454;
Best Local Similarity 20.9%; Pred. No. 0.0024;
Matches 64; Conservative 65; Mismatches 138; Indels 39; Gaps 11;
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```
QY 146 SSTVASOSANHTGTTSHRETQKAYL-----LAAGVIVCIYIICA 185
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 143 SANITRSSGKTKIVTSARTV--AYGVNFIILTSTPLVSTIGNQWTVAIIVGCFATIFT 200
| | | | | : : : : | | | | | : : : |
QY 186 VILILGVREOREPEYEAQOSEPIAYFGRGLRVMSHGPYKILITGFLTSLAPMLVEGNVL 245
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 201 WYTAFGIREKDNV-AKKKEKQGFQFINLKTWKPLRIVLLSMLVLELSGSIKNTISY 259
| | | | | : : : : | | | | | : : : |
QY 246 FCTYTLGFRNEFQ-NLLLAIMLSATLTIPWQWFLT-RFGKKTAVYVGI--SSAVPFLIL 301
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 260 YVKY--NFNAEMMIPVYSSVGMGASILGGIMSPFLTKLGRKNTALLGLLAGAAGSFLV 317
| | | | | : : : : | | | | | : : : |
QY 302 VALMESNLIIITYAVAAAGISVAAAFLLPWSMLPDVIDDHFHLKQPHFGTPIFFSVFV 361
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 318 L-LSYSSLPLMIVINFTISGIPDAGYITLTSWADCEVGEWKTG--KRSEGMIFSLNIF 374
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
QY 362 FTTFASGVSLGISTLSLDFAGYQTRGCSQPERVFTLN---MLVTMAPIVILILGLLFLK 418
| | | | | : : : : | | | | | : : : |
| | | | | : : : : | | | | | : : : |
Db 375 KSKTASAGSLSGILYIAYIGY----TANESQSAFTLNGIHLIOTLVPCAIVILSFILLR 430
| | | | | : : : : | | | | | : : : |
QY 419 MYPIDE 424
| | | | | : : : : | | | | | : : : |
Db 431 RYNLSE 436
| | | | | : : : : | | | | | : : : |
```

RESULT 11

```
Q8X673
ID Q8X673 PRELIMINARY; PRT; 457 AA.
AC Q8X673;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Glucuronide permease.
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